

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWAGGFACTV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351 CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRE KDNHNPRDFL ARTQGTAAARA
51  HAAQONGFEA FAPFAAAVLTA AHATGNAGQA TVNTLAGLFI LFRFAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVAA*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10          20          30          40          50          60
m156.pep      MTFAYWCILIACLLPLFCAAYAKKAGGFREKDNHNPRGFLAHTOGAAARAHAAQONGFEA
               |||||
a156          MTFAYWCILIAYLLPLFCAAYAKKAGGFREKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10          20          30          40          50          60

              70          80          90          100          110          120
m156.pep      FAPFAAAVLTAHATGNAAQSTINTLACLFI LFRFAFIWCYIADKAAMRSLMWAGGFACTV
               |||||
a156          FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWVGGFVCTV
              70          80          90          100          110          120

m156.pep      GLFVAAAX
               |||||
a156          GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgcctgcgc cgcaattgC gCgGgcggcg
51  ttgcgAAATg GGgcgagacg tGCGggCGGC GGCGgCgatA Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGATTg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCGGCGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401 GCTACCGTTT GGGGAGGCA GCGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTTCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLKRYI KRGRKIGVYW
  51 PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMERERKR
 101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGGC
  51 TTCGCAAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACC
 101 ACCTGCTCAA ACGTTATATT AAAAAAGGGC GGAAATCGG CGTGATTGG
 151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
 201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGGGCGGGA
 251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAAACAAGA ACGCAAGCGC
 301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
 351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTGGGTATG GACAGGCTGG
 401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
 451 ATGAAATACC GTTTCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
 501 GTTGGTGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGGACGGTT
 551 TTGTGTCGGA GCGGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAATV KINHLLKRYI KKGRKIGVYW
  51 PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
 101 GRAKLHVPQF AGRKKRVHDL NLLVLPVVG DRLGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMGRDVRAAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRMWFTYPERGMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRMWFTYPERGMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	NLLVLPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	NLLVLPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
  51 CGCGCAGATG GGGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAACC
```



```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACC GCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGGCGA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTCAGGC AAAAACCCTG GCGGTGGGCT TTGCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACC GCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

a157.pep

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYP ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
	: : :: : :					
a157	MRNEEKHALRRELRRARAQM GHQGRLAAGQTINRLLKRYIKRGRKIGVYWPMGKELRLDG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAEYLYPYIEPRSRMWFTYPADGVKQERKGRAKLHVPQFAGRKIRVHDL					
	: : : ::					
a157	FVRAAQKRGAKLYLPYIEPRSRMWFTYPESGMERERIRGRAKLNVPQFAGRKIRVHGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLLVFVGM DRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
	:: :: : :					
a157	SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL					
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

g158.seq

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CCGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGcTc
151 aACCGACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTGCGCGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
 851 TATTTTGGGA TTTTGTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
 901 AATACCAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep
 1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRR AQRILQEMAAA ETEMLAVHEV PQGVLRVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR
 301 NTK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
 151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG GTTTGAGCGT GGATTCCGCG
 301 AGCTTGCCGG TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
 351 ACGCTATCCG CATATCCGAC TTTGCTCGT TTCTTCCGAA GGCTATATCA
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
 451 GATTCCGGGC TCGCTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
 601 ACATGGGCGG TTTTAGATGC GCAGGGGAAAT CCCTATAAGA TTTACCCGCA
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA
 751 GGAAAGTTAA TTCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
 851 TATTTTGGGA TTTTGTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep
 1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRR AQRILQEMAAA ETEMLAVHEI PQGVLSVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSRFRVIAS EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
 251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
g158	MKTNSEELTVFVQVVESGSFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRR AQRILQEMAAAEETEMLA VHEI PQGVLSVDSAMP MVLHLLAP LAAKFNERYP					
g158	EEGAQYFRR AQRILQEMAAAEETEMLA VHEV PQGVLRVDSAMP MVLHLLAP LAAKFNERYP					
	70	80	90	100	110	120

	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTTHPFNAVYYSDKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTCAAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCCG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGCACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCCG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTATAGATG	GCAGGGAAT	CCCTATAAGA	TTTCACCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTGGGA	TTTTTTAGTG	GAGGAACTGG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRR	QRILQEMAAA	ETEMPLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSSE	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRRQRILQEMAAEETEMPLAVHEIPQGVLSVDSAMPMVLHLLAPLAAKFNERYP					
a158	EEGAQYFRRRQRILQEMAAEETEMPLAVHEIPQGVLRVDSAMPMVLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

	130	140	150	160	170	180
m158.pep	HIRLSLVSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSNKTTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCcCaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCCCGCTCC  GGTGCGGCAC  GGCATATATG  TATTTTCCCG
201 GCGCGGCTTG  GGTCATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTTCATATG  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAACTCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGGTTGC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCCGCTTC  AAAAGCCAA
701 TCGGACTCAG  CCCGCACGCC  TTTGTGAACC  ATATCCGCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCCGATTTCG  GTTTTGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTTCG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGOWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLESEK
151 PLTGTVSUVN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAATGAG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCAGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTC

```

```

501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAGGCG CGTTGCTGCT GAAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      MDILDKLVDL AQLTGSADVQ CLLGGQW--- HETLQREGLV HIVTAGSGYL CIDGETSPRP
          10      20      30      40      50

          70      80      90     100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      VGTGDIVFFP RGLGHVLSHD GKYGESLQPD IRQNGTFMVKQCGNGLDMSL FCARFRYDTH
          60      70      80      90     100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMVNALSSVLL VLILRAYLEQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SEKPLTGTV SVVNALPSVLL VLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      DKDVELSGVL KGWQDKRLGH LIQKVIDKPE DEWNIDKMVA AANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      PHAFVNHIRL QKGALLLKKTPDSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
1 ATGGACATTC TGGACAAACT GGTGATTTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```

101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGC GGCA ACGGACAGGA TATGAGCCTG TTTTGC GCGC GTTTCGCTA
351 CGACACCCAC GCCGATTTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGT
801 CGCACTGTCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKROYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP

          70      80      90     100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          70      80      90     100     110     120
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ
          130     140     150     160     170     180
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLES KKPLTGTV SMVNALSSVLL VLILRAYLEQ

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDMV AAANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240
a160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDMV AAANMSRAQLM RRFKSRVGLS

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKROYHVS PGQYRKEGGQ
          250     260     270     280     290     300
a160      PHAFVNHIRL QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKROYHVS PGQYRKEGGQ

m160.pep KX
          ||
a160      KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1   ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 CCGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTCGTCggt ttggcgacg
601 Ctgaccggt ggCACaccct GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcy cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCTCGC tttcctaTAt gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTTTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1   MDTAKKDILG SGWMLVAAAC FTMNVNLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTRFTRPHW KNHLNRSMVG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL GEELFWOEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1   ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTG TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTT GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCTCGC TTTCTATAT GACCGCTGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTTTCTG GGCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1   MDTAKKDILG SGWMLVAAAC FTIMNVNLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RDXFTRPHW KNHLNRSMVG TGAMLLLFYA VTHLPLATGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE

```

151 TAAGLAGG AMGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
 201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
 251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
 301 *

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLFSTVALGAAAVL					
	: : : : :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLFSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMVGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	: : : : :					
g161	RRDTFRTPHWKNHLNRSVMVGTGAMLLLFYAVTHLPLTTGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	: : : : :					
g161	RISVYTQAVLLLGFGVLLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	: : : : :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	: : : : :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

a161.seq

1	ATGGATACCG	CAAAAAAGA	CATTTTAGGA	TCGGGCTGGA	TGCTGGTGGC
51	GGCGGCCTGC	TTTACCATTA	TGAACGTATT	GATTAAAGAG	GCATCGGCAA
101	AATTGCCCT	CGGCAGCGGC	GAATTGGTCT	TTTGGCGCAT	GCTGTTTTCA
151	ACCGTTGCGC	TCGGGGCTGC	CGCCGTATTG	CGTCGGGACA	CCTTCCGCAC
201	GCCCCATTGG	AAAAACCACT	TAAACCGCAG	TATGGTCGGG	ACGGGGGCGA
251	TGCTGCTGCT	GTTTACGCG	GTAACGCATC	TGCCTTTGGC	CACCGGCCTT
301	ACCCTGAGTT	ACACCTCGTC	GATTTTTTTG	GCGGTATTTT	CCTTCCTGAT
351	TTTGAAAGAA	CGGATTTCGG	TTTACACGCA	GGCGGTGCTG	CTCCTTGCTT
401	TTGCCGGCGT	GGTATTGCTG	CTTAATCCCT	CGTTCCGCAG	CGGTCCAGGAA
451	ACGGCGGCAC	TCGCCGGGCT	GGCGGGCGGC	GCGATGTCCG	GCTGGGCGTA
501	TTTGAAAGTG	CGCGAACTGT	CTTTGGCGGG	CGAACCCGGC	TGGCGCGTCC
551	TGTTTTACCT	TTCCGTGACA	GGTGTGCGCA	TGTCATCGGT	TTGGGCGACG
601	CTGACCGGCT	GGCACACCCT	GTCCCTTTCCA	TCGGCAGTTT	ATCTGTCTGT
651	CATCGGCGTG	TCCGCGCTGA	TTGCCCAACT	GTGATGACG	CGCGCCTACA
701	AAGTCGGCGA	CAAAATCACG	GTTCCTCGC	TTTCTATAT	GACCGTCGTT
751	TTTTCCGCTC	TGCTGCGCG	ATTTTTTCTG	GCCGAAGAGC	TTTTCTGCA
801	GGAAATACTC	GGTATGTGCA	TCATCATCCT	CAGCGGTATT	TTGAGCAGCA

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51 TVALGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVMSSVWAT
201 LTGWHTLSFP SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLFSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLFSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGFGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTTt
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGGTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCAGC
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTGTAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTG TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTtTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTTCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCAGC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCCG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCACG AGCAGGTGGA ATGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1 MVILTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFSEF
51 LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLF AAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQO QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFASQ
201 LGAGLQEMGW IAENSFGVQV LIIAAVMSLA VVSAISGVGK GVKVLSEINL
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFSWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQDEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTTAC CGAGTTCAGC TGGTTTTATG TTTTAACGTT TTCCATTTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```

```

m163.pap
1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51 LGFLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYAGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATTEFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVK GKVKLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITSRDKGLSA PRWQADMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADMKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQGQEL
651 MAHEOVELAE *

```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m163.pep	MVILTTLFFVCVLVVLVLTVPDQVQMWL	DRAKEVIFTEFSWFYVLTF	SIFLGFLLILSVS			
g163	MVILTTLFFVCVLVVLVLTVPDQVQMWL	DRAKEVIFTEFSWFYVLTF	SIFLGFLLILSVS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDEDVPEFGFLSWL	AMLFAAGMGVGLMFFGVAEPL	MHYFSDITAGTPEHRQQ			
	:					
g163	GLGNIRLGRDEDVPEFGFLSWL	AMLFAAGMGVGLMFFGVAEPL	MHYFSDITVGAPEHRQQ			
	70	80	90	100	110	120
	130	140	150	160	170	180

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLOEMGWIENSFSVQVLLIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLOEMGWIENSFSVQVLLIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRSLFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVRIMSQTQEODILKFLKHTASPMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTGC TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCGTTCACG
401 CTTGGTTCGGT GTACGGTACG ATTGCATTGG CTTGGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAAGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCGT TTTTGCTGCT GTTTTTTGT TGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTCC GCGACAACAT AGGGAACATC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTTGTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACTTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELOR ELSEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF LGFLILSVS
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a163       MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF LGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA EPLMHYFSDI TAGTPEHRQQ

```

```
m163.pep      X
               |
a163           X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTCC CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTGGAC GGACAAAAGC
151 CGGCCGGCCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCCG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTCTg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacg TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTTCAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCGTC GTGCCGTC AATACGCCGA ACGGCAAAAG
751 GCGCGCAGCG TCGGCATCCC CTGCCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGGCGA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTC GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCGATTTTC TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAAGAT TTGATTATTT
1001 CCAAAGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GGCGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGG
1151 GCGAGGACGA aatccgcgcg caccTGCGTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGROPR INDLAHIIYT SGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKQNVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCTGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251 TACCGATGAA CACATTTTTG AAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCGCCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTTC CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCG CCGTTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA

```

```

951  CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGCTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACCTGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNK NGTAVFDGKE KTAYRALKQE AEVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQTLKLRATV FLGVPAIYTA MSKAKIPWYF RWFNRIRLFI SSGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVGELIVRG GSVMRGYLNM PAATDETIVN GWLKTGFVFT
401 IDEGDFIFIV DRKKDLIISK QONVYPREIE EEIYKLDAVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          10      20      30
          120     130     140     150     160     170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          40      50      60      70      80      90
          180     190     200     210     220     230
m164.pep  SGTGHPKGALISYANLFANLNGIERIFKISKRDRFIVFLPMFHSFTLTAMVLLPIYMAC
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          100     110     120     130     140     150
          240     250     260     270     280     290
m164.pep  SIILVKSVPFSNVLKQTLKLRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          160     170     180     190     200     210
          300     310     320     330     340     350
m164.pep  LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSGIPLPGLEAKAVDEEL
g164      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
          220     230     240     250     260     270
          360     370     380     390     400     410

```



```

m164.pep  VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      VEVPRGEVGEIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      LIISKQNVYPREIEEEIHKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAAACGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTTG AAAAAACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTTG
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCGTGTTCAT AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTGCG CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTG AGTGCCGCGC GGCGAAGTGG GCGAAGTATG
1101 CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTFVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQALLKRATV FLGVPAYITA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLIISK GQNVYPREIE EEIYKLDVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA

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501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIQVKGFDTV					
a164	: : : : : : : : : :					
	10	20	30	40	50	60
	MNRTYANFYEMLTAAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIQVKGFDTV					
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	: : : : : : : : :					
	70	80	90	100	110	120
	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGLGRQPRINDLAHIIYTS GTTG					
a164	: : : : : : : : :					
	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPDGEMAEAGDAFFEDVRRFPEKPDGLGRQPRINDLAHIIYTS GTTG					
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKRDREIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	: : : : : : : : :					
	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKRDREIVFLPMFHSFTLTAMVLLPIYMACSIILV					
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKTRATVFLGVPPIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	: : : : : : : : :					
	250	260	270	280	290	300
	KSVFPFSNVLKQALLKTRATVFLGVPPIYTAMSKTKIPWYFRWFNRIRLFISGGAPLAEQT					
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
a164	: : : : : : : : :					
	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEVAVDEELVEVPR					
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
a164	: : : : : : : : :					
	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	: : : : : : : : :					
	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	: : : : : : : : :					
	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GGCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC  GTTTGTCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAagat  gTGGCGTTGG  AATCGTCAAA  cGCGTGGAAC
151 AACGcCGgca  CGGGGCATTc  CGcGCTGTGc  GAATTGAACT  AtgcgccGCT
201 GGGtgcgga  ggcgtcatCA  ATCCGGCGCg  cgCCCTGAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGcga  cgctgGTCGC  GGAAGGCAAG
301 TTGGAagaCA  ATTCCTTCAT  CAATGCcgtg  ccgcatatGT  Ctttggtgat
351 gAacgaagac  cactgCCgtt  acCTGCAAAA  ACGCTATGAT  GTGTTTAAAA
401 CGCAGAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CtccgCTGAT  TATGCGCGGC  CGGgacgaaA  ACCAACCCGT
501 CGCCGCCAAC  TATTCCGCCG  Aaggcacgga  tgtcgATTTC  GGACGGCTGA
551 CGCGCCAGAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCAGGTTC
601 AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCAGACTG  GCAGCTCACC  CTCGCCACCC
701 GCTTCCTCTT  CCTCGGCGCG  GGCGGCGGCG  CACTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTACCCG  TGTCGGCCTT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAAAC  AACGCCAAAG
851 TGTACGGGCA  GGCTTCCGTC  GGCGCGCCGC  CGATGTCCGT  CCCGCACCTC
901 GACACACGCA  ACGTAGACGG  CAAACGACAC  CTTATGTTTC  GTCCTTACGC
951 AGGTTTCCGT  TCCAACCTCC  TCAAGCAAGG  CTCGTTTATG  GATTTGCCGC
1001 TGTCCATCCA  TATGGACAAC  CTCTATCCTA  TGCTGCGCGC  CGGCTGGGCG
1051 AATATGCCGC  TGACCAAATA  CcTGCTGGgC  gAaTTGCgtt  aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSALC  ELNYAPLGAD  GVINPARALN  IAEQFHVSRQ  FWATLVAEGK
101 LEDNSFINAV  PHMSLVMNED  HCRYLQKRYD  VFKTQKLFEN  MEFSTDNRKI
151 SDWAPLIMRG  RDENQPVAA  YSAEGTDVDF  GRLTRQMVKY  LQKGKVKTEF
201 NRHVEDIKRE  SDGAWVLKTA  DTRNPDWQLT  LRTRFLFLGA  GGGALTLLOK
251 SGIPGKGYG  GLPVSGLFFR  NSNPETAEOH  NAKVYGOASV  GAPPMSPVPHL
301 DTRNVDGKRH  LMFGPYAGFR  SNFLKQGSFM  DLPLSIHMDN  LYPMLRAGWA
351 NMPLTKYLLG  ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GGCGGCGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTGTCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAAGAT  GTGGCGTTGG  AATCGTCAAA  CGCGTGGAAC
151 AACGCGGCA  CGGGGCATTc  CGcGCTGTGc  GAATTGAACT  ATGCGCCGTT
201 GGGTGCAAA  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGCTGGTTCG  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTGAT
351 GAATGAAGAC  CATTGTTCTT  ATCTTCAAAA  ACGTTATGAC  GCGTTTAAAA
401 CCCAAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CTCCGCTGAT  GATGCGCGGC  CGGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TACTCCGCCG  AAGgTACGGA  TGTGATTTTC  GGACGGCTGA
551 CGCGCCAAAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601 AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCGACGG  GCAGCTCACC  CTCGTACCC
701 GCTTCCTCTT  CCTCGGCGCG  GGCGGCGGCG  CGCTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTCCCG  TGTCGGCCTT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAAAC  AACGCCAAAG
851 TGTACGGGCA  GGCTTCCGTC  GGCGCGCCGC  CGATGTCCGT  CCCGCACCTC
901 GACACACGCA  ACGTGGACGG  CAAACGCCAC  CTTATGTTTC  GCCCTTACGC
951 AGGCTTCCGT  TCCAACCTCC  TCAAGCAAGG  CTCGTTTATG  GATTTGCCGC
1001 TGTCCATCCA  TATGGACAAC  CTCTATCCTA  TGCTGTGCGC  CGGCTGGGCG
1051 AATATGCCGC  TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSALC  ELNYAPLGAN  GIIDPARALN  IAEQFHVSRQ  FWATLVAEGK
101 LEDNSFINAV  PHMSLVMNED  HCSYLQKRYD  AFKTQKLFEN  MEFSTDNRKI
151 SDWAPLMMRG  RDENQPVAA  YSAEGTDVDF  GRLTRQMVKY  LQKGKVKTEF

```

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTREFLFLGA GGGALTLLQK
 251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSPVPHL
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLCAGWA
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

m165.pep	10	20	30	40	50	60
	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	10	20	30	40	50	60
	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
m165.pep	70	80	90	100	110	120
	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	70	80	90	100	110	120
	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165.pep	130	140	150	160	170	180
	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
g165	130	140	150	160	170	180
	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLMRGRDENQPVAANYSAEGTDVDF					
m165.pep	190	200	210	220	230	240
	GRLTRQMVKYLGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLT LRTREFLFLGA					
g165	190	200	210	220	230	240
	GRLTRQMVKYLGKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDWQLT LRTREFLFLGA					
m165.pep	250	260	270	280	290	300
	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
g165	250	260	270	280	290	300
	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSPVPHL					
m165.pep	310	320	330	340	350	
	DTRNVDGKRHLMFGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	310	320	330	340	350	360
	DTRNVDGKRHLMFGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTGTCTCA	AAGAACTCGA	ACCGTCTTGG	GAAATCACCC
101	TGATTGAACG	CTTGAAGAT	GTGGCGTTGG	AATCGTCAAA	CGCGTGAAC
151	AACGCCGGCA	CGGGGCATTC	CCGCTGTGC	GAATTGAAC	ATGCGCCGT
201	GGGTGCAAAT	GGGATTATCG	ATCCGGCGCG	CGCCCTCAAT	ATTGCCGAAC
251	AGTTTCATGT	CAGCCGCCAG	TTTTGGGCGA	CGTTGGTCGC	GGAAGGCAAG
301	TTGGAAGACA	ATTCCTTCAT	CAATGCCGTG	CCGCATATGT	CTTTGGTGAT
351	GAATGAAGAC	CATTGTTCTT	ATCTTCAAAA	ACGTTATGAC	GCGTTTAAAA
401	CCCAAAAAT	TTTTGAAAAT	ATGGAATTTT	CCACCGATCG	GAACAAAATT
451	TCCGATTGGG	CTCCGCTGAT	GATGCGCGGC	CGGGACGAAA	ACCAACCCGT
501	CGCCGCCAAC	TACTCCGCGG	AAGGCACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAAAT	GGTGAAATAT	TTGCAGGGCA	AGGGCGTAAA	AACCGAGTTC

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGAGCA AACCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTG GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA
```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```
a165.pep
  1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
 51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVKY LQKGVCATFEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFER NSNPETAEOH NAKVYGQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMRLAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKID
401 SEKGVVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165/a165 99.7% identity in 356 aa overlap

```
          10          20          30          40          50          60
m165.pep  MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a165       MAEATDVVLVGGGIMSATLGVLVLLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC
          10          20          30          40          50          60

          70          80          90          100         110         120
m165.pep  ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a165       ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED
          70          80          90          100         110         120

          130         140         150         160         170         180
m165.pep  HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDF
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a165       HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDF
          130         140         150         160         170         180

          190         200         210         220         230         240
m165.pep  GRLTRQMVKYLQKGKVKTEFNHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a165       GRLTRQMVKYLQKGKVKTEFNHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
          190         200         210         220         230         240

          250         260         270         280         290         300
m165.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFERNPNPETAEQHNKAVYGQASVGAPPMSVPHL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a165       GGGALTLLQKSGIPEGKGYGGFPVSGLFERNPNPETAEQHNKAVYGQASVGAPPMSVPHL
          250         260         270         280         290         300
```

```

          310      320      330      340      350
m165.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSILMDLPLSIHMDNLYPMLCAGWANMPLTK
          |||||
a165      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSILMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
          310      320      330      340      350      360

a165      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
          370      380      390      400      410      420

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAc
151 AACGCGGca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccgac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctggtCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGA AAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcGTGAT TATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACC GCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCGCACCC
701 GCTTCTCTTT CCTCGCGCGC GCGCGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCCCTACGC
951 AGGTTTCCGT TCCAAC TTCC TCAAGCAAGG CTCGTTTATG GATTTGCCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGTG GGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTtt gCCTCCCTGC TGgaatacta cccGaggcag acccGACGAc
1151 tgg tactac cagcgaggnc acGCGTcata tcattanata tgactCgaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgtcgcggcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttgaaaa gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDNRKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTROMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTREFLFLGA GGGALTLLQK
251 SGIPGKGYG GLPVSGLFRR NSNPETAEOH NAKVYGOASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPQ TRRLVLITQX TRHIIXYDSK
401 LRLVLQLYEIV PRDARSRIE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAc
151 AACGCGGca CGGGGCATTC CGCGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTTCG GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAAACT TTTTGA AAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACC GCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCTACCC
701 GCTTCTCTTT CCTCGCGCGC GCGCGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG

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851 TGTACGGGCA GGCTTCCGTC GGC GCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGAGCA AACCCCGACG
1151 ACTGGGAACAT CATCACCGCA GGGCAACGCG TCCAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGCG
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTAA
```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMRGR RDENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPGKGYG GFFPVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSVPHL
301 DTRNVGKRHL MFPGPYAGFR SNFLKQGS LM LPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
g165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
g165-1	ELNYAPLGADGVINPARALN	IAEQFHVSRQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDNRKISDWAPLMRGR	RDENQPVAAANYSAEGTDVDF			
g165-1	HCRYLQKRYDVFKTQKLFEN	MEFSTDNRKISDWAPLMRGR	RDENQPVAAANYSAEGTDVDF			
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQGGKGVKTEF	NRHVEDIKRES	SDGAWVLKTADTRNPDGQLT	LRTRFLFLGA		
g165-1	GRLTRQMVKYLQGGKGVKTEF	NRHVEDIKRES	SDGAWVLKTADTRNPDWQLT	LRTRFLFLGA		
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPGKGYGG	FVPVSGLFFRNSNPETAQEH	NAKVYQASVGAPPMSVPHL			
g165-1	GGGALTLLQKSGIPGKGYGGL	PVSGLFFRNSNPETAQEH	NAKVYQASVGAPPMSVPHL			
	310	320	330	340	350	360
m165-1.pep	DTRNVGKRHLMFPGPYAGFR	SNFLKQGSMDLPLSIHMDN	LYPMLCAGWANMPLTKYLLG			
g165-1	DTRNVGKRHLMFPGPYAGFR	SNFLKQGSFMDLPLSIHMDN	LYPMLRAGWANMPLTKYLLG			
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLLEYYPEAN	PDWELITAGQRVQIIKKD	SEKGGVLQFGTEIVAHADGS			
g165-1	ELRKTKEERFASLLEYYP	QTRRLVLITQXTR-HIIXYDS	-KLRVLQLYEIVPRDARSR			
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA
:
g165-1 ILERRGASRXALISADDTAPSAPVLESVX
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
1 ATGGGTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTTCG GGAAGGCAAG
301 TTGGAAGACA ATTCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACATTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGCGTAAA AACCGAGTTC
601 AACGCCCAGC TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCGC CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGCCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACGCG CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTATGTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCATTATG GATTGTCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGGCA AACCCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TCAAAATCAT TAAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTG GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCCAC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALE ELNYAPLIGAN GIIDPARALN IAEQFHVSQ FWTALVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKGD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

a165-1.pep	10	20	30	40	50	60
m165-1	10	20	30	40	50	60
a165-1.pep	70	80	90	100	110	120
m165-1	70	80	90	100	110	120
a165-1.pep	130	140	150	160	170	180
m165-1	130	140	150	160	170	180
a165-1.pep	190	200	210	220	230	240
m165-1	190	200	210	220	230	240


```

a165-1.pep  GRLTRQMVKYLGKGKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
m165-1      GRLTRQMVKYLGKGKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSVPHL
|||||
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
|||||
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
|||||
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
|||||
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
|||||
m165-1      YTAKVLDIX

```

a165-1/p33940

```

sp|P33940|YOJH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF_ID:o372#5; similar to [SwissProt Accession Number
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct
identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

```

Query: 3  EATDVVLVGGGIMSATLGVLKLELPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
+ TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63  NYAPLGGANGIIDPARALNIAEQFHVSQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSISIEKAVAINAEAFQISQFWAHQVERGLRTPRSFINTVPHMSFVWGEDN 149

Query: 122  CSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDFG 181
++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150  VNFLRARYAALQQSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQKVAATRTEIGTDVNYG 209

Query: 182  RLTRQMVKYLGKG-VKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
+TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210  EITRQLIASLQKKSNFSLQLSSEVRALKRNDNTWTVTVDLKNGTAG-NIRAKFVFIGA 268

Query: 241  XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASVGAPPMSVPHL 300
Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269  GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVNVNHLAKVYGKASVGAPPMSVPHI 328

Query: 301  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329  DTRVLDGKRVVLFPGFATFSTKFLKNGSLWDLMSSTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389  QVNLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRD AEKGGVLR LGTEVVS DQQT 448

Query: 421  XXXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

```

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLKVFVGDRVSSPQWQATLKAIVPSYGRKLNQDVAATERE 508

Query: 479 IAYTAKVLDI 488

+ YT++VL +

Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq

```

1 atggcgggcgg cggaaataaa acgccccctc gctgtcgatt tccagcacat
51 agcgtccggt ctgcacggcg gcatagccgc ttttgctgc ctgatagggg
101 tgcagggcgg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
151 ggcgatattg cccaccagtt tggcaaacaa ggtatggcac acgccgtttt
201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
251 acgacggcgt ccaagtcggt gggatgctt ccggtcagcc ggacggcggt
301 ttgttccggc aagcctttaa tccgataact gatttgtttt ttgccgtcgt
351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
401 ttgtcgatgt atttgacttt gaaaaccggt ttcggcgcg cttgtgcccgc
451 attttgccgc tgttcgcgcg tattttcgga ttgcccagc gcggcaagca
501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaac tggcaggcgg
601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac
651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgc ttttgccgcg
701 ctgcctgcaa aatctcttcg atttgcaag gattagaggt caatgcgttg
751 tag
  
```

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep

```

1 MAAAEIKRPL AVDFOHIA SV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFOV GMLSGQPDGV
101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDF ENRFRALCR
151 ILRLFRIRIFG FAAGGKQQA AOHGKRYFOH SALLMVSOCR LKRLKRGR
201 RFGRHWVYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL
251 *
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq

```

1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT
51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCTGC CTGATAGGGT
101 TGCAGGCGCG CATGCGAAAC TAGGTAATCC GTCAGTTGTC CGCCGTCTTC
151 GGCGATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
201 CTGCCCAACC TGCCCGACTG TCCTTATCAT CGGTTTCCAT ACATTTGCCG
251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAAT CCAAACCGGC AATCGCCGTA
401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
451 GTTTTGCGGC TGTACCGCCG TATTTWCGGA TTTGCCGCaC GGCaArgCAG
501 CAGGCAGCCG CCAATACGG CAAAARAwGT wTTCAGCATT CCACaYTCCT
551 GATGGTTTCA AAATGCCGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC
601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
651 ATAATTGCGG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC
701 TCTTCGATTT GCGAAGGGTC GCGGTCAGC TCGTTGTAG
  
```

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep

```

1 MAAAEIKRPF AVDFOHIA SV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFOVA GMLADQSDNI
101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRALYR
151 VLRLYRRIXG FAATAXQQA AQYKXXXQH STXLMVSKCR LKRGRRRFRGR
201 HRVHFNRMPT TASGTLSNNS RASLRAFAAP ACKISSICEG SAVSSL*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

	10	20	30	40	50	60
m204 . pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
g204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNQVISQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
m204 . pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
g204	GMAHAVFRPARRRVLSVGFHTFADDGFQVVGMLSGQPDGVLFRQAFNRITDLFFAVVGFA					
	70	80	90	100	110	120
m204 . pep	FAALSQIQTGNRRIVDIYDFENRFRRLALYRVLRLYRRIXGFAATAQQAAAQYKXXXQH					
g204	FATLSQSQTGNRRIVDVDFENRFRRLALCRILRLFRIFGFAAGGKQAAAQHGKRYFQH					
	130	140	150	160	170	180
m204 . pep	STXLMVSKCRLK---RGRRRFGRHRVHFNGRMPTASGTLNNRSLRAFAAPACKISS					
g204	SALLMVSKCRLKCRLLKGRRRFGRHWVYFNGRMPTASRTLSNNRSLRAFCAPACKISS					
	190	200	210	220	230	240
m204 . pep	ICEGSAVSSLX					
g204	ICEGLEVNAL					
	240					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204 . seq

```

1  ATGGCGGCGG CGGAAATAAA ACGCCCCCTC GCTGTCGATT TCCAGCACAT
51  AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTGCTGTC CTGATAGGGT
101 TGCAGGGCGG AATGCGAAAT CAGGTAATCC GTCAGTTTGC CGCCGTCTTC
151 GGCGATATTG CCCACCAAGT TGGCAAACAA GGTATGGCAC ACGCCGTTTG
201 CCGCCCAGCC CGAAGGCGCG CCCTTTCCGT CGGTTTCCAT ACATTGCGCG
251 ACGACGGCTT CCAAGTCGTT GGGATGCTTG CCGGTCAGCC GGACGACGTT
301 TTGTTCCGGC AAGCCTTT ..
351 .....
401 .....
451 .....
501 .....
551 .....AAGAG GTTCGGACGG
601 CATTGGGTTT ATTTCAACGG GCGGATACCG ACCGCATCAC GTACTTTGCC
651 CAATAATTCG CGTGCTTCTT TACGCGCTTT TTGCGCGCCT GCCTGCAAAA
701 TCTCTTCGAT TTGCGAAGGG TCGGCGGTCA GCTCGTTGTA G

```

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204 . pep

```

1  MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIQLGGMRN QVIRQFAAVF
51  GDIAHQFGKQ GMAHAVCRPA RRRALSVGFH TFADDGFQVV GMLAGQPDDV
101 LFRQAF....
151 .....KREGR
201 HWVYFNGRIP TASRTLPNNS RASLRAFCAP ACKISSICEG SAVSSL*

```

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSFGFHTFADDGFQVVGMLAGQPDVLFROAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTNRRIVDIYDFENRFRRLYRVLRLYRRIXGFAATAXQQAQYKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKGRRRFRGRHVRHFNGRMPASGTLNNSRASLRFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNSRASLRFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

g205.seq

```

1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcggaata tccgaaaata cggcggaaca gccgcaaat gcgcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttggggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaaagga cgcgccttcg ggctgggagg aaaacggcgt
351 gtgccatacc ttgtttgcca aactgggtgg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgacag aacggacgct atgtgtctga
501 aatcgacagc gagggggcgt tttatttccg ccgccgccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

g205.pep

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNTA EDGGKLTIDY ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

m205.seq

```

1  ATGCTGAAwA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CCGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGA AGCCGTCAGC GGCAAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGCGAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTTCGATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCCGC CGCCGCCATT ATTGA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m205.pep		MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNAVQSAPKPVFKVIYIDNTA	AGLDLGQSSE				
						:	
g205		MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSA	PKPVFKVKYIDNTA	AGLALGQSSE			
		10	20	30	40	50	60
		70	80	90	100	110	120
m205.pep		GKTNDGKKQISYPIKGLPEQN	VIRLIGKHPGDLEAVSGKCMETDDK	DS	PAGWAENG	VCHT	
					:		:
g205		GKTNDGKKQISYPIKGLPEQNA	VRLTGKHPNDLEAVVGKCMETDGKD	APSGWAENG	VCHT		
		70	80	90	100	110	120
		130	140	150	160	170	180
m205.pep		LFAKLVG	NIAEDGGKLT	DYLVSHAALQ	PYQAGKSGYAAVQ	NGRYVLEIDSEGA	FYFRRRH
				:	:	:	:
g205		LFAKLVG	NIAEDGGKLT	DYLI	SHSALQ	PYQAGKSGYAAVQ	NGRYVLEIDSEGA
		130	140	150	160	170	180
m205.pep		YX					
g205		Y					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

a205.seq	(partial)	1	2	3	4	5
1	TCCGAACCTC	TTAAAGGCTT	GCCGGAACAA	AACGTCGTCC	GGCTGACCGG	
51	CAAGCATCCC	AACGACTTGG	AGGCCGTCGT	CGGCAAATGT	ATGGAAACCG	
101	ACGGAAGGG	CGCGCCTTCG	GAGTGGCGCT	CAACACCGCT	TGCGCATACC	
151	TTGTTTGCCA	AAC TGGTGGG	CAATATCGCC	GAAGACGGCG	GCAAAC TGAC	
201	GGATTACCTG	ATTTTCGCAT	CCGCCCTGCA	ACCCTATCAG	GCAGGCAAAA	
251	GCGGCTATGC	CGCCGTGCAG	ACCGGACGCT	ATGTGCTGGA	AATCGACAGC	
301	GAGGGGCGCT	TTTATTTCGG	CCCGGCCCAT	TATTGA		

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

a205.pap (partial)

1	SEPLKGLPEQ	NVRLTGKHP	NDLEAVVGKC	METDGKGAPS	GWAANGVCHT
51	LFAKLVGNIA	EDGGKLT DYL	ISHSALQPYQ	AKSGGYAAVQ	NGRYVLEIDS
101	EGAFYFRRRH	Y*			

m205/a205 88.3% identity in 111 aa overlap

```

      50          60          70          80          90         100
m205.pep    KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPPIKGLPEQNVRIRLIGKHPGDLEAVSGKC
a205                                     | |:| ||||| :|| |||:|||| |||
                                      SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
                                           10          20          30

      110        120        130        140        150        160
m205.pep    METDDKDSPAGWAENGVCHTLFAKLVGNI AEDGGKLT DYLVSHAAL QPYOAGKSGYA AVO

```

g205-1.seq (partial)

1	ATGCTGAAAA	TACCTTTTGC	CGTGTGGGCG	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAATA	CGGCGGAACA	GCCGCAAAAT	GCGGCACAAA
101	GCGCGCCGAA	ACCGGTTTTC	AAAGTCAAAT	ACATCGACAA	TACGGCGATT
151	GCCGGTTTGG	CTTTGGGACA	AAGTAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAAGGCTT	GCCGGAACAA	AACCGCGTCT
251	GGCTGACCGG	AAAGCATCCC	AACGACTTGG	AAGCCGTCGT	CGGCCAAATG
301	ATGGAACCGG	ACGGAAGGGA	CGCGCCTTCG	GGCTGGGCGG	AAAACGCGCT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACCTGA	TGATTACCTG	ATTTCGCATT	CGGCCCTGCA	ACCTGATCAG
451	GCAAGCAAAA	GCGGCTATGC	CGCCGTGCAG	AACGGACGCT	ATGTTGTGGA
501	AATCGACAGC	GAGGGGCGCT	TTTA		

g205-1.pep (partial).

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALQSSE GKTNDGKKQI SYPTKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNIA EDGGKLTDL IHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAF

```

m205-1.seq..

```

1   ATGCTGAAAA CATCTTTTGC CGTATTGGGC GGCTGCCTGC TGCTTGCCGC
51  CTGCGGCAAA TCCGAAAATA CGGCGGAACA GCGCAAAAC GCGGTACAAA
101 GCGCGCGCAA ACCGGTTTTT AAAGTCAAAT ATATCGACAA TACGGCGATT
151 GCGCGTTTGG ATTTGGGACA AAGCAGCGTA GGCAAAACCA ACGACGGCAA
201 AAAACAAATC AGTTATCCGA TTAAGGCTT CCGCGAACAA AATGTTATCC
251 GACTGATCGG CAAGCATCCC GCGCAGTTGG AAGCCGTACG CGGCAATGTG
301 ATGGAACCGG ATGATAAGGA CAGTCCGGCA GGTGGGCGAG AAAACGGCGT
351 GTGCCATACC TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG
401 GCAAACTGAC GGATTACCTA GTTTCGCTAG CCGCCCTGCA ACCCTATCAG
451 GCAGGCAAAA GCGGCTATGC CGCGTCGACG AACGGACGCT ATGTGCTGGA
501 AATCGACAGC GAAGGGGCGT TTTATTTCCG CCGCGCCCAT TATTGA

```

m205-1.pgp

```

1  MLKTSFAVLG GCLLLAACGK SENTAEQPN AVQSAPKPVF VKYIDNTAI
51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSPA GWAENGVCHT LFAKLVGNI A EDGKGLTDYL VSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*

```

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAACGKS	SENTAEQPQNAAQSA	PKPVFKVKYIDNTA	IAGLALGQSSE		
m205-1	MLKTSFAVLGGCLLLAACGKS	SENTAEQPQNAVQSA	PKPVFKVKYIDNTA	IAGLDLGQSSE		
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQ	NAVRLTGKHPNDLEAV	VGKCMETDGKDAPSG	WAENGVC	HT	
m205-1	GKTNDGKKQISYPIKGLPEQ	NAVRLTGKHPNDLEAV	VGKCMETDDKDS	PAGWAENGVC	HT	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

m205-1/a205-1 89.0% identity in 109 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 715>:

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

g206.pep
1 MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKOTVROIO AVRISHIGRT

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
 101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
 151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

m206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGSAaA ATCCCGGAcA GCCGcYTCaA
 351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
 451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep..
 1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
 101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
 151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

m206.pep	10	20	30	40	50	60
	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	70	80	90	100	110	120
	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	130	140	150	160	170	
	LVFFNTGGAHRYSHVGLYIG NGEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTEX					
g206	IVFFNTGGAHRYSHVGLYIG NGEFIHAPSG GKTIKTEKLS TPFYAKNYLGAHTFFTE					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCTTAA
 351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
 401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
 451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
  1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYK	NALNVKLPRTARDMAAASRK	IPDSRXKAGD		
a206	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYK	NALNVKLPRTARDMAAASRK	IPDSRLKAGD		
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
a206	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEKLS	TPFYAKNYLGAHTFFTEX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
  1 atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
 51 tgctgcggtt gatgtgccac tgctggcgca tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcggttccag ataggttttg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt ctgcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtcgtcgccg tatttttctt tgatggtctg cagttcgggt gcggcgccac
501 gcattttcgc catcgaaagg taggaggcgt tggtaaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttgtgc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctcgg gatgtttgcg
701 ataacggatg tggtttgagg accggcatac aggttgaccg ccattttcgg
751 ttttggtccc cgggttgagg tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
  1 MLRHLGNDFA LGALFFDAV DVPLLGDGQE VVDHPVENQT GREEEHEDGE
 51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVG VG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRQTAA QRVDLFVFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEP EERRCEPVYFT VFVCQLQVVG DVCNDGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
 51 GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTCGCC TGCATCGGGT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGCGGCACG
501 CATTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGCGA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGGAGAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTGCGGG TTTTGCGGAT GTATTGCGCC
951 TCGGATTGTC CGGATTGTC ATCGTCGTCC AAGTCGGAAG AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQEP EERGGEVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTLVLYSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

```

m209/g209
10 20 30 40 50 60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
g209 MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEEHDGENQRHDFHHFR
10 20 30 40 50 60
70 80 90 100 110 120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVAEVEGNPTQPRCLAQFYGGEQCPIQSDG
g209 LHRVGRRRVQIGLGEHRCRHNDGQDVVGVAEVEGNPAQPRCLAQFYGGEQCPVQADEG
70 80 90 100 110 120
130 140 150 160 170 180
m209.pep DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
g209 DLQQRQTAAQRVDFLVFEKLHHRLLLRHTVVAVFFFDGLQFGCGGTHFRHRTVGGVGQW
130 140 150 160 170 180
190 200 210 220 230 240
m209.pep IQYGFDDDGXNDNRPAVADDVVQLVQEP EERGGEVYFAVVGQLQVVG DVCDDGCGLR
g209 IQYGFDDDGQNDDCPAPVADNVVQLVQEP EERRCEPVYFTVVFCQLQVVG DVCNDGCGLR
190 200 210 220 230 240
250 260 270 280 290 299
m209.pep AGVEVDGGGFGF-APFWMAAKGTLTLVLYSLRLMSMLHSPAAQTLCLPLGWRIQVDMK
g209 :::|| | | | |
TGIVDRHFRFWPPGWDSG
250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CCACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```

51  TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201 GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451 GTCGTCGCGG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC CCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCACT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTTGTGCGC GATGTTTGGC
701 ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801 CAGCTTGTCG TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCAATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGBA TGTATTCGGC
951 CTCGGATTGG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1  MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLOQHRQAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCDNGCGLW AGVEVDGGFG
251 FAPFWIAAKG TLTLVLYSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQFVG VLRMYSASDL PDLASSKSE KLTFWKLPSPG V*

```

m209/a209 95.6% identity in 341 aa overlap

```

              10      20      30      40      50      60
m209.pep      MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
a209           MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR
              10      20      30      40      50      60

              70      80      90      100     110     120
m209.pep      LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG
a209           LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAAEVGNPTQPRCLAQFYGGEQCPIQSDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m209.pep      DLQQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
a209           DLQQHRQAAAQRVDFLVCVKLHHGLLLRHTVVAVFLFDGLQFGRGGTHFRHRTVRGVGQW
              130     140     150     160     170     180

              190     200     210     220     230     240
m209.pep      IQYGFDDDGXNDNRPAVADDVVQLVQEPPEERGGEVPYFAVVFGQLQVVGDVCDGCGGLR
a209           IQYGFDDDGXNDNRPAVADDVVQLVQKPEGGGEPVYFAVVFGQLQVVGDVCDNGCGLW
              190     200     210     220     230     240

              250     260     270     280     290     300
m209.pep      AGVEVDGGFGFAPFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW
a209           AGVEVDGGFGFAPFWIAAKGTLTLVLYSLSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW
              250     260     270     280     290     300

              310     320     330     340
m209.pep      CSIMPSQFVGVLRLMYSASDLPDLASSKSEKLTFWKLPSPGVX

```

a209 CSIMPSQPVGLRMYASDLPDLASSKSEKLTFWKLP SGVX
310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```
g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttgggcg tgggtgctgat aatcagggtt
101 agtttttgga aggaaacctg attgtagtcg gcgcgtccgg gcgtgcogct
151 gtaacggtag ccgtggcgca attcagagct gctgttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgcctcgccc gttttgttcc
251 tgttcgcgca ggaacaggtt ttctcatgat cgggattcgg tgtcaaaggt
301 ttcgacgaaa taaacctctg cgttgcgctt gcccaagtta ttgaactcgc
351 cggcttccac caaagacaat tcctgcttct gcttcaaaat ttcggcatat
401 tcgcgggtgc gcaagctctg ccacggtatc acccaaagct gcatgacggc
451 aatcaggatg gcaaacggca cggcaaactg catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag
```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

g211.pep

1	MLRIAAANQL	GGRNGAAVGN	GVDKFGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	<u>VTVA</u> VAQFER	AFVVLQREVT	<u>FFGEDDVVAA</u>	VFVLFAQEQV	FHDAGFGVKG
101	FDEINPAVAL	AQVIELAGFH	<u>QROFLLLLON</u>	FGIFAAALC	PRYHPKLHDG
151	NQDGKRHGKL	HDGAYPLFQR	QSAG*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```
m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTTCGATG AGTTTGGGCG TGGTGTCTGAT AATCAGGTTG
101 AGTTTTTTGGA AGGAAACTCG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGCTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTGT TCGTTTCAGCG
201 AGAAGTTACC TTCTTTGCGC AAGATGATGT TGTGCGCCGC TGTTTTGTCC
251 TGTTGCGGCA GGAACAGGTT TTTTCATGAT CCGGATTCCG TATCGAAGGT
301 TTCGACAAAA TAAACCTCTC CGTTGCGCTT GCCCAAAC TGTAACCTCGC
351 CTGCCTCCAC CAAAGACAA TCTTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAAACGGC CGGCAAACAT CATACCGGG CGTATCCATT
501 GTTTCATATG CAATCCGCAG GATAG
```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

m211.pep

1	MLRVA	AAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFLEG	<u>NL</u>	<u>IVVGASGR</u>	<u>AA</u>
51	<u>VTVA</u>	<u>VAQFER</u>	AQVVVQREV	TFGEDDVAA	VFVLFAQEQV	FHDAGFGIEG		
101	<u>FDKINPAVAL</u>	<u>ACTVELAC</u>	<u>LDLH</u>	<u>QRQFLL</u>	<u>LLQD</u>	FSVFAAAXLC	PRYHPKLHDG	
151	NQNGKR	HGKL	HHRAYPLFC	QSAG*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```
m211/g211
```

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNVDFEGRGADNQVEFLEGNLIIVVGASGRAAVTVAVAQFER					
	:	:	:	:	:	:
g211	MLRIAANQLGGRNGAAGVGNVDKFGRGADNQVEFLEGNLIIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60

	70	80	90	100	110	120
m211.pep	AFVVVQREVTFEGEDDVVAAVFLFAQEQQVFHDAGFGIEGFDKINPAVALAQTVELACL					



```
a211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTTGGA AGGAACACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTTG TCGTTCAGCG
201 AGAAGTTACT TTCTTTGGCG AAGATGATGT TGTCCGCCCC GTTTTGTCC
251 TGTTGCGGCA GGAACAGGTT TTTCATGATG CCGGATTCCG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAAC TGGAACCCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAAACGGC CGGCAAAC TGATACCGGG CGTATCCATT
501 GTTTCAAATGC CAATCCGCGG GATAG
```

```
a211.pep
1  MLRVAANQL  GGRNGTAVGN  GVDEFGRGAD  NQVEFLEGNL  IVVGASGRAA
51  VTVAVAQFER  AFVVVQREVT  FFGEDDVVAA  VFVLFAQEQV  FHDAGFGIEG
101  FDKINPAVAL  AQTVEPACIL  QRQFLLLQLD  FSVFAAA*LC  PRYHPKLHDG
151  NQNGKRHGKL  HHRAYPLFOC  OSAG*
```

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLGHHRAYPLFQCQSAGX					
	130	140	150	160	170	

```
g212.seq (partial)
      1  atggacaatc tcgatatgga cggcattccc gacatccgca cactcgacca
     51  aaccatccgc aaacacgcac acccgctcaa cctgattgtc tgccctccccg
    101  ataatcagat tcccgatttt caaacgcac aagatgcttc ggactcggaa
    151  tgccgtctga agcaccgttt ggatcaggca acccagtgcc tccagttcga
    201  cagcatcaac ctcatcgaac acatcctgcc cgatgtccgc ttctggctgg
    251  ttcccccttc acgcaccgcg cgctgacg acacttcca ccacatttcc
    301  tggcagaccg aagccattcc gcaaacggaa agcaagtcg acaaacctg
    351  gtttgcactt ccacaaacat ccgaacggaa aaaaccggaa cagctcctc
```

```

401 tcatcgggtgc aggcattgcc ggcgcatcga cgcgccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccggacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattggggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccg aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtec
851 gcaccctcct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcactactg caccggcgcg cacagccctt
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacccggc tcacaccgtc caccctgtt tccgaacaac tgcgttgccg
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcaactgt
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcgca agcattggca caccctaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQTIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL POTSERKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACCT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GGCGCGGCAA CCGCCCACGC CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTGCGCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTTCGTC
851 GCACCCTCCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGGACCACT TTCCCTAGT CGGCGCACTC
1351 GCGGACATTG CCGCCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAACCTACCG ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGAATCGCCA CCGCCCCCAT CTGCGCCGCC

```

1501 GmCAwTGcAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHLRLDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN ROGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDS PDHPLVLGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII	CLPDNQIPDFQTAQDASDAE	CRLKHLRLDQA
g212	MDNLVWDGIPDIRTLDQTIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSE	CRLKHLRLDQA	
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESK	PKPWFAL	
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRLHEHFHHISWQTEAIPQTESK	SDKPWFAL	
m212.pep	POTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNROGLLYAKIS		
g212	POTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNROGLLYAKIS		
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH		
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH		
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP	LIGLHEDTPL	
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL		
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNLAAALPLRQIRG	QTGLTPSTPF	
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNLAAALPLRQIRG	QTGLTPSTPF	
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAE	EEASNRQALAH	LNPALESSE

```

g212      |||||
          SEQLRCAVSGESYISPSWHGLHCYGFIPNSSNTGWNEAEEASNRQALAHLPALAESL
          370      380      390      400      410      420
          430      440      450      460      470      480
m212.pep  FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
          |
g212      F

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>>:

```

a212.seq
1 ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AACCATCCGC AAACACGGAC ACCCGCTCAA CCTGATTGTC TGCTCCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ACCGATGCC TCCAGTTCGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCGGC CGCCTGCACG AACACTTCCA CCACATTTC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCG ACAAACCTG
351 GTTTCGACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGGCGATATC GCGCGCGCAA CCGCCACGC CTTAGCATCA
451 TACGGCATT TCCGTTACCGT ATTGGAAGCC CGAAAAGCCG CTTAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAAC CGAACTGCTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACATA TCCTGCCCGC ATCCGAAACC TGGGGCGGCA AGGCGATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCATACAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACGCA GGCAGAAGCC
751 GAAAAAATCG CCGCATCCCC TCTGAACACG CCCTACGCCG AACCATTATG
801 CGGACTGTTT TGGCAGTACG GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 CGGCCCTCCT CAGCCATCCG CTCATTGGAC TACACGAAGA CACACCGTTA
901 ACCGACATTT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCTC GCCACCCTGC CCCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCGTTGCGC
1101 CGTTTTCAGG GAAAGTACA TCAGCCCGTC GTGGCAGGCA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCG ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCTTAGT CGGCGCACTC
1351 GGCGACATTG CCGCTATGCA ACAAACCTAC CGCAAACCTG CGCTGGACAA
1401 AAATATCGC ATCGATGCCC CCTGCCCGTA CCTGCCCAAT GCCTACGCCA
1451 ACACCGCCCC CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCCGCC
1501 CCGGTTGCAG CCGAAATCCT AGGCTTGCCC CATCCCCTCT CAAAACGCCT
1551 GCGCCACGCC CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

```

a212.pap
1 MDNLAWNGIP DIRTLDQITR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKPKDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAQAAGASN RGQLLYAKIS PHDTEQTELL LAGYGYTKRL
201 LGHILPESET WGGNGIIHNL YSRTEQQRNH ELGLQKHNNH LYRSITQAEAL
251 EKIAGIPLNT PYAEPLCGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTPL
301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYNISPSWHG LHCYGASFIP NSSHTGWNEA
401 EEASNRLQALA HLNPALESSEL FAANPNPQKH QGHAAIRCDS PDHPLPLVGAL
451 GDIAAMQQTY AKLALDKNYR IDANPCPYLPN AYANTANGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIIRA IVRRKDLTP*

```

m212/a212 93.7% identity in 539 aa overlap

```

      10      20      30      40      50      60
m212.pep MDNLVWDGIPDIRTLDDAIRKHAPPLNLIICLPDNPQIPDFQTAQDASDAECLRKHRLDQA
      |||:|:|||||:||||| ||||:|||||:|||||:|||||:|||||:|||||:|||||
a212      MDNLAWNGIPDIRTLDDQIRKHAHPLNLIVCLPDNPQIPNFQTAQDASDAECLRKHRLDQA

```


	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1   atgatacaaa agatatgtaa gctatttgtt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcttc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcagcg aaaggcggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaaag ggacggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaaggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

```

1  MIQKICKLFV LIVIFATSPA FALQSDSRFP IQIEADQGSF DQANQRTTFS
51  GNVIIROGTL NISASCVNVT RGRQRRRIRE GGRFARPLQP NVGRGQORDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQRQH
151 EIGCEIRFQN RQGQRRHPAF KHTKNRITPM PSETETQFRR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTGAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGGCGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGSF DQANQSTTFS
51  GNVVIRQGTI NISAARVNVT RGRQRRRIRE GGRFASPLQP DIGRRQRHGA
101 RTGKQRCLEI CRQHRSLNR* CQSTARRRRC RRCGDIQHQ NRSLYHQRQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

```

m214/g214

      10      20      30      40      50      60
m214.pep  MIQKICKLFVLIAFFSASPALQSDSRQPIQIEADQGSFDQANQSTTFSGNVVIRQGTI
          |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||
g214       MIQKICKLFVLIVIFATSPALQSDSRPFIQIEADQGSFDQANQRTTFSGNVIIROGTL
          10      20      30      40      50      60

      70      80      90     100     110     120
m214.pep  NISAARVNVTGRQRRRIREGGRFASPLQPDIGRRQRHGARTGKQRCLEICRQHRSLNRX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g214       NISASCVNVTGRQRRRIREGGRFARPLQPNVGRGQRDGARGKQRYLFLRRKHCRSDRQ
          70      80      90     100     110     120

      130     140     150
m214.pep  CQSTARRRCRRRCGDIQHQNRSLYHQRHKI
          |||:|||||:|||||:|||||:|||||:|||||
g214       CQSAARRRRCRRRCGHYLQHQNRSLYHQRQHEIGCEIRFQNRQGQRRHPAFKHTKNRITPM
          130     140     150     160     170     180

g214       PSETETQFRRHLPTMPRRDY
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGC.GGC AAAGGCGGCG AATCCGTGAG GCGGAAGGTT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GCGGCAAAG GCACGGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISAARVNVT RGXQRRRIE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLF I CRQHRSLNR* CQSTARRRC R RCGDYIQH Q NRSLYHQRH
151 KIRRKIRFQ I RQGRRYPAF EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

```

          10      20      30      40      50      60
m214.pep  MIQKICKLFVLIAFFSASP AFALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQGT L
          |||||||
a214      MIQKICKLFVLIAFFSASP AFALQSDSRQPIQIEADQGS LDQANQSTTFSGNVVIRQGT L
          10      20      30      40      50      60

          70      80      90     100     110     120
m214.pep  NISAARVNVT RGRQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNRX
          |||||||
a214      NISAARVNVT RGXQRRRIE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNRX
          70      80      90     100     110     120

          130     140     150
m214.pep  CQSTARRRCRRRCG DYIQHQNRS LYHQRH K I
          |||||||
a214      CQSTARRRCRRRCG DYIQHQNRS LYHQRH K I R R K I R F Q I R Q G R R Y P A F E Y A K I R I I P M
          130     140     150     160     170     180

a214      PSETXTWFG RHLPTEILKRY L X
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTTCGAAC
 51 TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGCCCC ATCCAAATCG
101 AAGCCGACCA AGGTTTCGCTC GATCAAGCCA ACCAAAGTAC CACATTTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTTCCG CCTCGCGCGT
201 CAACGTCACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTAGCCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAAA ACCGAAGTCT ATACCATCAA CGGCAGCACG
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGTGCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLFV LIVIFATSPA FALQSDSRP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISASRVNVT RGGKGGESVR AEGSPVRF S Q TLDGGKGTVR
101 GQANNVTYSS AGSTVVL TGN AKVQRGGDVA EGAVITYNT K TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGCG
 51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT

```

m214-1.pap

```

1  MIQICKLFLV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANOSTTFS
51 GNVVIRQGT L NISAARVNV T RGGKGGEVSR AEGSPVRF S Q TLDGGKGTVR
101 QOANNAVAY S AGSTVLTG N AKVQRGSDV A EGAVITYN T K TEVYTIISG S T
151 KSGAKSASK S GRVSVVIQ P STQSE*

```

		10	20	30	40	50	60
m214-1.pep		MIQKICKLFVLIAFFSASP	AFALQSDSRQPIQIEADQ	GSGLDQANQSTTFSGNV	VIIRQGT		
g214-1		MIQKICKLFVLIVIFATSP	AFALQSDSRRPIQIEADQ	GSGLDQANQSTTFSGNV	IIIRQGT		
		10	20	30	40	50	60
		70	80	90	100	110	120
m214-1.pep		NISAARVNVTRGGKGGES	VRAEGSPVRF	SQTLDGGKGT	VRGQANNVAYSSAG	STTVLTGN	
g214-1		NISASRVNVTRGGKGGES	VRAEGSPVRF	SQTLDGGKGT	VRGQANNVTYSSAG	STTVLTGN	
		70	80	90	100	110	120
		130	140	150	160	170	
m214-1.pep		AKVQRGGDVAEGAVITYN	TKTEVYTI	SGSTKSGAKS	ASKSRVSVVIQ	PSSTQKSEX	
g214-1		AKVQRGGDVAEGAVITYN	TKTEVYTING	STKSGAKS	ASKTGRVSVVIQ	PSSTQKTEX	
		130	140	150	160	170	

sp|P38685|YHBN_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_o185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

```

Query: 19  PAFALQSDSRQPIQIEADQGSLDQANQSTTFSGNVVIRQGTNLISAARVNVTR--GGKGG 76
          PAFA+  D+ QPI IE+DQ SLD      TF+GNV++ QGT+ I+A +V VTR  G +G
Sbjct: 24  PAFAVTGDTDQPIHIESDQQSLDMQGNVVFTFTGNVIVTQGTIKINADKVVVTRPGEQGG 83

Query: 77  ESVRAEGSPVRFQSQTLDGGKGTVRGQANNVAYSSAGSTVVLTGNAKVQRGGDVAEGAVIT 136
          E +   G P F Q D GK V G A + + Y A  VVLTGNA +Q+      +G IT
Sbjct: 84  EVIDGYGKPATFYQMQDNGK-PVEGHASQMHYELAKDFVVLTGNAYLQOVDSNIKGDKIT 142

Query: 137  YNTKTE 142
          Y  K +
Sbjct: 143  YLVKEQ 148

```

a214-1.seq

1	ATGATACAAA	AGATATGTAA	GCTATTTGTT	TTAATAGCAT	TTTTTTCGGC
51	GTCCCCCGCT	TTTGCCCTTC	AAAGGCAGCAG	CAGGCAGCCT	ATTCAGATTG
101	AGGCCGACCA	AGGTCGCTCT	GATCAAGCCA	ACCAAAGCAC	CACATTACGC
151	GGAAACGTCT	CTATCAGACA	GGGTACGCTC	AATATTTCCG	CGCCCGCGTT
201	CAATGTTTACA	CGCGGCGGCA	AAGGCGGCGA	ATCCGTGAGG	GCGGAAAGTT
251	CGCCAGTCCG	CTTCAGCGAG	ACATTGGACG	CGCGCAAAGG	CACGGTTCGC
301	GGACAGACCA	ACAACGTTGC	TTATTCTACT	CGAGGCAGCA	CCGTAGTCTT
351	AACCGGTAAT	GCCAAAGTAC	AGCGCGGCGG	CGATGTCGCC	GAAGGTGCGG
401	TGATTACATA	CAACACCAAG	ACCGAAGTCT	ATACCATCAG	CGGCAGCACA
451	AAATCCGGCG	CAAAATCCCG	TTCCAAATCC	GGCAGGGTCA	CGCTCGTTAT
501	CCAGCGTTCG	AGTACGCAAA	AATCCGAATA	A	

a214-1.pgp

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

51 GNVVIRQGTI NISAARVNV T RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
 101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLI	AFFSASP	FALQSDSR	QPIQIEAD	QGS	LDQANQSTTFSGNVVIRQGTI
m214-1	MIQKICKLFVLI	AFFSASP	FALQSDSR	QPIQIEAD	QGS	LDQANQSTTFSGNVVIRQGTI
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVNV	TRGGKGG	ESVRAEG	SPVRF	SQTLDGGK	GTVRGQANNVAYSSAGSTVVLTGN
m214-1	NISAARVNV	TRGGKGG	ESVRAEG	SPVRF	SQTLDGGK	GTVRGQANNVAYSSAGSTVVLTGN
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGGD	VAEGAVI	TYNTKTE	VYTISG	STKSGAK	SASKSGRVSVVIQPSSTQKSEX
m214-1	AKVQRGGD	VAEGAVI	TYNTKTE	VYTISG	STKSGAK	SASKSGRVSVVIQPSSTQKSEX
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq
 1 atgaaagtaa gatggcggta cgggaattgcg ttccattga tattggcgggt
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
 101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
 151 ttggacggaa ggcggtttga cgaacagggg tacttgaaag aacatttgag
 201 cgcgaaaggt gcgaaacagt ttcccgaaaa cagcgacatc cattttgatt
 251 agccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
 301 agcgatgaag ccgtttacca taccgaaaac aaacaggttc ttttataaaa
 351 caacgttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggttaaag
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc
 451 gatacgctg tcagtttcca atatggcgcg tcgcacggtc aggcgggagg
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
 551 aagccgcgat ttatgatata aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep
 1 MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPHLVFF QEGRLLYEVG
 101 SDEAVYHTEN KQVLFKNVNV LTKTADGRRQ AGKVETEKLN VDTESQYAQT
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
 101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG CGCGAAGGGC
 151 GCGAAACAGT TTCCGGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT
 201 CGTGTCTTTC CAAGAAGGCA GGTGTGTGTA CGAAGTCGGC AGCGACGAAG
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG
 401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGCGGGCGCG CATGACTTAC
 451 GACCACAWWA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)
 1 ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
 51 AKQFPENSDI HFDSPHLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNVNV
 101 LTKTADGKRQ AGKVEAEKLN VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/q215

```

m215.pep          10          20          30          40
                   SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
                   |||||:|||||
g215              MKVWRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTM DGLD GRRFDEQG
                   10          20          30          40          50          60

                   50          60          70          80          90          100
m215.pep          YLKEHLSAKGAKQFPSSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
                   |||||:|||||
g215              YLKEHLSAKGAKQFPENSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
                   70          80          90          100          110          120

                   110          120          130          140          150          160
m215.pep          LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHTGMLNFS
                   |||||:|||||:|||||:|||||
g215              LTKTADGRRQAGKVETEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYNNHKTGMLNFS
                   130          140          150          160          170          180

                   170
m215.pep          SKVKATIIDTKDMX
                   ||||:|||||
g215              SKVKAAIIDTKDM
                   190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCATTGA	TATTGGCGGT
51	TGCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCGACGCAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GCGGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTGTAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTCGACT
251	CACCGCATCT	CGTGTTCCTC	CAAGAAGGCA	GGTTGTTGTA	CGAAGTCGGC
301	AGCGATGAAG	CCGTTTACCA	TACCGAAAA	AAACAGGTTT	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAACACGGCAG	CGGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCCAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAAA	CAGGCATGTT	GAACTTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pap

1	<u>MKVRWRYGIA</u>	<u>FPLILAVALG</u>	<u>SLSAWLGRIS</u>	EVEIEEVRLN	PDEPQYTM DG
51	LDGRRFDEQG	YLKEHLS S KG	AKQFPES SDI	HFDSPHLVFF	QEGRLLYE VG
101	SDEAVYHTEN	KQVLFKNNV V	LTKTADGKRQ	AGKVEAEKLH	VDTESQYAQT
151	DTPVSFQYGA	SHQVAGGMTY	DHKTGM LNFS	SKVKATIIDYT	KDM*

m215/a215 98.3% identity in 173 aa overlap

```

                                10      20      30      40
m215.pep                      SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG
                                |||||
a215      MKVRWRYGIAFPPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMGDGLDGRRFDEQG
                                10      20      30      40      50      60
                                50      60      70      80      90     100
m215.pep      YLKEHLSAKGAKQFPSSDIHFDSPLHVFVQEGRLLYEVGSDAEVYHTENKOVLEKNNV

```

```

a215      |||||:|||||
          YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
          70      80      90      100      110      120

          110      120      130      140      150      160
m215.pep  LTKTADGKROAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
          |||||:|||||
a215      LTKTADGKROAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
          130      140      150      160      170      180

          170
m215.pep  SKVKATIYDTKDMX
          |||||:|||||
a215      SKVKATIYDTKDMX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtaccacgc gacgaaatca ccgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgc
101 ccgattcaac catggcgcg ccatgccgata tccacatcac cgcacgggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttgggcgt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgcccg cagcctcgcc
301 aaacgcctgc ttttgccgct tgccgacatt atgcacaaag gcggcgccct
351 gcccgcctgc cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaagg tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSSVPS DEITAIIPAL KRKDITLVC I TARP DSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAF TPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGAI VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGsACAAAA
101 ACTTCGTCCT TGCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGgCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTG TCCtGCTGCG CgcACGCGCG TTCACGCCCC
551 ACGATTTCGC CTTGAGCCAT CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAAAG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGGC
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

```

51  ITGMVKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLMG IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPTTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQRLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100      110      120
m216.pep      TMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVC
g216           ::|||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
              10      20      30
              130     140     150     160     170     180
m216.pep      TARPDSMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARAFTPDDF
g216           ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
              40      50      60      70      80      90
              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQRL
g216           || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

```

a216.seq
1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51  GCACACCGAA GCGGAAGGCT TGCGCGAAAT TGCGGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGGCGGAC GCGTTGTTGC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCCG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCAGCCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCGCTGG GGCTTGCCCC GACCACCAGC ACCACGCGCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGTGTCG CGCCCGCGCG TTCACGCCCG
551 ACGACTTCGC CTTGAGCCAC CCTGCCGCGA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCCTGC CTGCCGTCCG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

```

a216.pep
1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRVV
51  ITGMKSGHI GRKMAATMAS TGTPAFFVHP AEAHGDLMG IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAPTTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQRLKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHHPKT ISAERLATEA LKVMQANHVN

```


301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENKYLWAREVLHAEAEGLREIAAELXKNFVLAADALLHCKGRVITGMVKSGHI					
a216	MAMAGNEKYLWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVITGMGKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLGMIVDXDVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLGMIVDNDVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHTASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDSTMARHADIHTASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRKGVFTDGDRLRLFQECDNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
a216	DGQGRKGVFTDGDRLRLFQECDNFTGLSIDEVMHHPKTISAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGV LIGALNMHDL LAARIVX					
a216	GLLVTDADGV LIGALNMHDL LAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcgatg acggtttgtt gcggaactg tccgaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctgaggtt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgagg ttgccgcat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggaac aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgctgaca tctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgccgcgca tttctccgtc caatccccaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgg aaacggcgca acacggggcg ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttcagca agtcggacac gcaactccaa
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgata ggggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAFOQVGH ALQRIKKRLP AADFHVRNGI

```

201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGCGCGATG  ACGGTGTGCG  GCGGCAACTG  TCCGGAAAAT  TCGGCCAATT
51  CGGTTTCCGC  CTCCATTG  ACCCATTCGT  TTTCAAGGTT  TTGGACTGAC
101 TTTTGGTCAT  CGGCTTCAGC  TTGGAACAAT  GTTCAAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTGCGCGA  CCGTTGCGGG  CTGCCGCCAT  ATCCGTACAA
201 TATCCGTCAG  GGTTCGAGG  AAGGCGGCAA  AACGTCCGAA  CATGGCGGTT
251 TGATTACAGT  CGGCATACCA  CGCGCTGACA  TCCTGCCACA  TCGGATTGCC
301 GCCTTTGGGC  AGCATCCAGC  CCAATATCAT  GCGTTCCTACC  GCCTGCTTCC
351 AGGTGAACAG  CTGATCCGTG  CCGCCGCGCA  TTTCTCCGTC  CAAACCCCGAG
401 TGGACGTTCA  AATCGGCAAC  CATGTCGTGC  AAAAGCGGTA  AATCGTCCTC
451 AGTCAGTCCG  AAACGGCGCA  ACACGGGCGC  GGTTTCTAAA  AGCACAAAGCA
501 CTTTATCGAC  TTCAAATCGG  CTTTCCAACA  AGTCGAACAG  GCATGACAAA
551 GCATGAAACA  GCGGTTGGCG  GCGGCTGATT  TTCACGTCTG  ACACGGAATA
601 CGGCAATGCC  TGCGCACCgG  GctGCGCCTG  TCCGAACACG  GCTTCGATAA
651 AAGGCGTATA  GGATTCGATA  TTCGGGGTTA  A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL  SGKLRQFGR  LPFDPFVKV  LDxLLVIGFS  LEQCFKQIPA
51  TRHPFADRCG  LPPYPYNIRO  GFEEGGKTSE  HGGLIHVGIP  RADILPHRIA
101 AFGQHPAQYH  AFYRLLPGEQ  LIRAAAHFSV  QTPVDVQIGN  HVVQKRXLIVL
151 SQSETAQHGR  GFXXKXHFID  FKSAFQOQVEQ  AXQSMKQRLA  AADFHVXHGI
201 RQCLRTGLRL  SEHGFDKRI  GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

m217.pep	10	20	30	40	50	60
	MADDGVRRLSGKLRQFGRLPFDPFVKVLDXLLVIGFSLEQCFKQIPATRHFPADRCG					
g217	MADDGLLRLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHFPADRRR					
	10	20	30	40	50	60
m217.pep	70	80	90	100	110	120
	LPPYPYNIROGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
m217.pep	130	140	150	160	170	180
	LIRAAAHFSVQTPVDVQIGNHVQKRXLVLSQSETAQHGRGFXXKXHFIDFKSAFQOQVEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQOVGH					
	130	140	150	160	170	180
m217.pep	190	200	210	220		
	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRRIGFDIRGX					
g217	ALQRIKKRLPAADFHVNRNGIRQCLRAGLRLSEHGFKRRIGFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG  ACGGTGTGCA  GCGGCAACTG  TCCGGAAAAT  TCGGCCAATT
51  CGGTTTCCGC  CTGCCATTG  ACCCATTCGT  TTTGAGGCT  TTGGACTGCC
101 TTTTGGTCAT  CGCCTTCGAC  TTGGAACAAT  GTTCAAGCA  AATCCCGGCA
151 ACGCGCCACC  CATTGCTCAA  CCGTCGCAGG  TTGCCGCCAT  ATCCGTACAA

```

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTTCACG GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGT CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC CGCGCCG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

a217.pep

```

1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCFKQIPA
51 TRHPFVNRRR LPPYPYNIRQ GFEEGGKTSE QGGLVHVGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHPPFADRCG					
a217	VADDGVQRQLSGKLRQFGFRLPFDPFVFEALDCLLVIAFDLEQCFKQIPATRHPPFVNRRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m217.pep	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
a217	LPPYPYNIRQGFEEGGKTSEQGGLVHVGIPRADPLPHRIA AFGQHPAQYHAFYRLLPGEQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFXKHKHFIDFKSAFQQVEQ					
a217	LIRAAAHFSVQTPADVQIGNHVQKRQIVLSQSEMAQHGRGFXKHKHFIDFKSAFQQVEQ					
	130	140	150	160	170	180
	190	200	210	220		
m217.pep	AXQSMKQRLAAADFHVXHGIRQLRTGLRLSEHGFDKRRI GFDIRGX					
a217	AXQSMKQRLSAAADFHIRNGIRQLRAGLRLSEHGFDKRRI GFDIRGX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

g218.seq

```

1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgcccg
51 caatcagggg tggatcaca ctatggatga aatccacggc gatatgatgc
101 tcggtgcccg aggcgattat cttttggaaa cggcagcttc actgaccatt
151 attatggttg tcagcggctt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tggtgccgga
251 atctgcacgg cgcgtttgga acttgggtgt cgttgatttt actgttggtc
301 tgctgtcgg gtattgcttg ggcaggtatt tggggcgcca aattcgtgca
351 ggcttggaat cagttcccgc ccggcaaatg ggggtgtcgaa ccgaacccc
401 tttcaatcgt gccgaccac gccgaggtat tgaatgacgg caaggttaag
451 gaagtgccgt ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccaataac attggaaacc
551 gtcgaccgtt tcgcgcggga aatcggtttc aaagggcggt atcagttgaa
601 tttgcccaca gccgaggacg ggggtatggac tttgtcgag gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

g218.pep

```

1 MVAVDPTYAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAG NRFQALSVE
 201 FAQRRGRGMD FVAGFYEL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCCGG
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
 101 TCGGTGCGGC AGGCGATTAT CTTTGGGAAA CGGCAGCTTC ACTGACCATT
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGC GCGGCAT
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAr GGC GCGTCT TGGTGGCGGA
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTTC
 301 TGCCTGTCGG GTATTGCTTG GCGGGTATT TGGGGCGGCA AGTTCGTACA
 351 GGCTTGGAGT CAGTTCCTTG CCGGTAAATG GGGTGTGCGA CCGAACCCCG
 401 TTTTCAGTCGT GCCGACCCAC GCGGAGGTAT TGAATGACGG CAAGGTTAAG
 451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG
 551 TCGACCGCTT TCGCGCGnGA AATCGGTTTC AAAGGGCGTT ATCAGTTGAA
 601 TTTGCCCAA GCGGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep
 1 MVAVDPYTAK VVSTMPRNQG WYTMDEIHS DMMLGAAGDY LLETAASLTI
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQALSVE
 201 FAQRRGRGMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

m218.pep	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYTMD	EHSDMMLGAAGDYLLETAASLTI	IMVVSGLYLW			
g218	MVAVDPYTAKVVNTMPRNQGWYHTMD	EHGDMMLGAAGDYLLETAASLTI	IMVVSGLYLW			
	10	20	30	40	50	60
m218.pep	70	80	90	100	110	120
	WVKRRGIKAMLLPSKGXARSWWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQRGIKAMLLPPKSRARSWWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
m218.pep	130	140	150	160	170	180
	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWVLELTPMPVSGTTVGKDGINPDEPMT					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKEVPWILELMPMPVSGTTVGGENINPTEPNN					
	130	140	150	160	170	180
m218.pep	190	200	210			
	LETVDRFARXNRFQALSVEFAQRRGRGMDFVAGFYEL					
g218	IGNRRPFRAGNRFQALSVEFAQRRGRGMDFVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGC GCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGC GCGTCTT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTC
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCGA CCGAACCTTG
401 TTTCAGTCGT GCCGACCCAC GGCAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGCGGTT ATCAGCTGAA
601 TTTGCCCAAA GCGGAGGACG GCGTATGGAC TTTGTCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPPVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQRLSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMD	EHSDMMLGAAGDY	LLETAASLTI	IMVVSGLYLW		
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEI	HSMDMMLGSTGDY	LLETAASLTI	IMIISGLYLW		
	10	20	30	40	50	60
m218.pep	WVKRRGIKAMLLPSKXARSWWRNLHGT	FGTWVSLILLF	CLSGIAWAGI	WGGKFVQAWS		
a218	WVKRRGIKAMLLPPKGRARSWWRNLHGAF	GTWVSLILLF	CLSGIAWAGI	WGGKFVQAWS		
	70	80	90	100	110	120
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDG	KVKEVPWVLELTP	MPVSGTTVGK	DGINPDEPMT		
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDG	KVKEVPWVLELTP	MPVSGTTVGK	DGINPDEPMT		
	130	140	150	160	170	180
m218.pep	LETVDRFARXNRFQRLSVEFAQRRGR	RMDFVAGFYEL				
a218	LETVDRFARXNRFQRLSAEFAQRRGR	RMDFVAGFYEL				
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```

g219.seq
1   atgacggcaa ggttaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt ggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaaccgtc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcgttatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtgcgaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtag agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatttatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggg ggagcgtggt ggcgaacgct gtgttctgcc
401 ttgccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaacgcg
451 cgtccgtccg gcgtggcggg cattgttcct ccggcgcaaa aaatcaaaact
501 gcccgtctgg tgggcgatgg cattgccgct gctgttgatt gcactgcttt
551 tcccagaccg cgtgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaata ga
  
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```

g219.pep
1   MTARLRKCRG FWSLCLCLSQ GRLVVKALT PPSITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV VFCLAVIFIG ISGCVMWWR
151 RPSGVAGIVP PAQKIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```

m219.seq
1   ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACyGt gGCGAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCCTTT GCCGACCGCA
251 CGGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTG GCGCAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTGCG GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```

m219.pep
1   MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTSRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWWR
151 RPTGAVGIVP PAQVKLPVW WMMALPLLAI ALLFPTSLLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

```

m219/g219
      10      20      30      40      50      60
m219.pep MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPS TALRGEIGFKGRYQLNLPKG
g219      MTARLRKCRGFWSLCLCLSQGRLVVKALT PPSITLETVD RFAREIGFKGRYQLNLPKG
      10      20      30      40      50      60
      70      80      90     100     110     120
m219.pep EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFM AASIALHMG T
g219      EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFM AASIALHMG T
  
```

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVKL PVWMMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMMWKRRPSGAVGIVPPAQKIKLPVWWMALPLLII					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWFK					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
  1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
 51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101  GATGACATTG GAAACCGTCG ACCGTTTTGC GCGG.GAAAT CGGTTTCAAA
151  GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201  GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251  CGGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301  GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351  TATGGGGACT TTGGGCTGGT GGAGCGTGTT GGCGAACGTT TTGTTCTGCC
401  TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451  CGTCCGTCCG GCGCGGTGGG CATGGTTCGG CCGGCGCAAA AAATCAAGCT
501  GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551  TCCCGACCGC GTTGCTTGCC ATTGCCGTA TTTGGCTGTT GGATACGCTG
601  CTGTTGTTCG GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
  1  MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTR*HWKPS TVLRXEIGFK
 51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101  DDYNPFQKFM AASIALHMG LWWWSVLANV LFCLAVIFIG ISGCVMMWKR
151  RPSGAVGMVP PAQKIKLPVW WAMAVPLLI ALLFPTALLA IAVIWLLDTL
201  LLSRIPVLRW WFK*

```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFQKFMAASIALHMG					
	: : : :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFQKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVKL PVWMMALPLLAI					
	: : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPSGAVGMVPPAQKIKLPVWWMAMAVPLLI					
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFVKX					
	: : : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFVKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```

g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaatc adatcgacgc tgacggattt gaaccttgcc
101 tcacggggcg catcgatgac ttctttggtt tcttcgtagc tttggatgcy
151 gttgactgcc gccctgcaact tggggtcgaa atcctgaatg ccgacgctca
201 tgcggttgaa gccgagtctg ccgagcatga ggacgggtgc gcggtgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcggcg cggcttttgt ctttggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcgg
551 ttgtttaa

```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```

g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKGRR AAEEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAVFVGD DFVAAAVVAD GVAKRNVNVK GKRFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```

m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTGCGCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGAAGAC
301 ACGTTCGATC TGTTGCTCGC TCAAAAAGGt GCGTGCCcCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```

m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DFFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAVFVG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

```

m221/g221
10 20 30 40 50
m221.pep  MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDFFGFFVTLDAVDRRLHFGVE
g221      MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE
10 20 30 40 50 60
60 70 80 90 100 110
m221.pep  ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-
g221      ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR
70 80 90 100 110 120
120 130 140 150 160 170

```


507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFFVFGDDFVAAAVVADGVAERNVNVK
             |||||
g221        AAEEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAFFVFGDDFVAAAVVADGVAERNVNVK
             130      140      150      160      170      180

m221.pep    GKRFVX
             |||||
g221        GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1   ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTGGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACCTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1   MVVLMRLSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH AVEAESAEHED GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFFKF DVGIGAAFFV
151 GDDEFVAAAVV ADGVAERNVN VKGKRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

m221.pep    10      20      30      40      50      60
             MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVEILNADAH
             |||||
a221        10      20      30      40      50      60
             MVVLMRLSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVEILNADAH

m221.pep    70      80      90      100     110     119
             VEAESAHEHEDGVAADFARVDFDGVFAGGD*LEMFAHYHAEDTFDLFVAQKGA-CPAEVQLG
             |||||
a221        70      80      90      100     110     120
             VEAESAHEHEDGVAADFARVDFDGVFAGGD*LEMFAHYHAEDTFDLVVAQKGRRAAAEVQLG

m221.pep    120     130     140     150     160     170
             KLVPSVQMWSEQFHFFFKIFDVGIGAAFFVFGDDFVAAAVVADGVAERNVNVKGKRFVX
             |||||
a221        120     130     140     150     160     170
             KLVPSVQMWSEQFHFFFKIFDVGIGAAFFVFGDDFVAAAVVADGVAERNVNVKGKRFVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1   atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51  ttctgatggc gaattggctt ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggtc atcgaagccg aaacgggcgg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcggtt ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgtc gagcagctct tgttcactga tctctttgcg
301 ccagtatttt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

1 MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA
51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLLAQVFGNV EQLLFTDLFA
101 PVFFLGEFQF TEGADTREAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

```
m223.seq
1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTGCAAC CATTTGGTCA
51 TTTTCGATAGC GAATTTGGTCT TTGTTACCGC AGCGCCAGTTG GAAGAATTGT
101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCsCTAC
201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTTCCAG TTTTCTCGC
251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC
301 CAGTATTTT CTTGTGCGAA TTTCAATTCG CGGAAGGCGC CGACACGCGG
351 GAAGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep

1	VEFRHQVVVV	GVEPFGHFDS	ELVFVTARQL	EELFQRQVLA	VEAEAGGNRA
51	GGDLQVEDVV	VESEIXYGNE	<u>IGVGSDLVFP</u>	<u>VFLAQVFSNS</u>	QQFLLDFFA
101	PVFFLCEFOF	AEGADTRE*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

```
m223/g223
```

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDDV					
	: : : : : :					
g223	MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLAIEAETGGNRARGYLQVEDVM					
	10	20	30	40	50	60

	70	80	90	100	110	120
m223.pep	VESEIXYGNEIGVGS DLVPVFLAQVFSNSQQFLLADFFAPVFFLCE FQFAEGADTREAX					
	: :					
g223	VESEITYSNVISVRSSLVFPVFLAQVFNVEQLLFDTDFAPVFFLG EFQFT EGADTREAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

```
a223.seq
1 GTGGAATTCa GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTTGGTCA
51 TTTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
101 TCCAAAGATA GGTTTTGGCT TCGCAAGCCG AAGCGGGCGG GAATCGCGCC
151 GGTGGCGGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA
201 CGGCAACGTA ATCGGCGTTG GCAGCGGCCT GGTGTTTCCA GTTTTTCTCG
251 CGCAAGTCTT TAGCAACAGC CAGCAATTCT TGCTCGCTGA TTTCTTTGCG
301 CCAGTATTTT TCTTGTGCGA ATTTCAATTC GCGGAAGGCA CCGACACGCG
351 GGAAGCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pap

1	VEFRHQVWVV	GVEPFGHFDS	ELVFVTARQL	EELFQR*VLA	VEAEAGGNRA
51	GGDLQVEDVV	VESEIAYGNV	<u>IGVGSGLVFP</u>	<u>VFLAQVFSNS</u>	QQFLIADFFA
101	PVFFLCEFOF	AEGTDTREA*			

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVVGVEPFGHFDSELVVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
a223	VEFRHQVVVVVGVEPFGHFDSELVVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYNEIGVGSDDLVPVFLAQVFSNSQQFLLADFFAPVFFLCEFQFAEGADTREAX					
a223	VESEIAYGNVIGVSGSLVPVFLAQVFSNSQQFLLADFFAPVFFLCEFQFAEGDTDREAX					

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag tttgccgaag acgaacagcc cgtttttacc
151  gtcaaccgag cccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcatcggcag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcgcc acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcg cacgtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451  cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcgccgcg cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgcccgc cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIARYYGG TSVSTGFDSCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNPDSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTCAAACC CGGCAGTTTG GCGGGTTTGG TGGCTGAWGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101  TTCTCAGACA GTTGCCGAA GACGAACAGC CCGTTTTACC CATCAACCGA
151  GCCCCGCCCG GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201  GGGGCTTAAC GAACAGCCCG TTTTACCGGT CAACCGAGTC CCGCCCCGGC
251  GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301  CAGCCCGTTT TACCCGTCAA CCGAGCCCCC GCGCGCGGG CCGGCAATGC
351  CGACGAATC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401  ACGGCGGCAC ATCGGTTTCT ACCGGTTTGG ACTGCAGCGG CTTTCATGCAG
451  CACATCTTCA AACCGGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501  ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551  ATATGGTGTT TTCCGCACG CTCGGCGGCA GCCGCATTTC CCATGTGCGA
601  CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CCGGGGAAAAA
651  TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701  TCGCCCGCCG GGTCAGAAA AACGACCGT CCGCTTTCT GAACCTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101  QVLPVNRAP ARRAGNADEL IGNAMLLGI AYRYGGTSVS TGFDCSGFMQ
151  HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRISHVG
201  LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

```
m225/g225
10 20 30 40 50
m225.pep FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g225 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
```

510

```

      10          20          30          40          50          60
m225.pep  60      70      80      90      100     110
NADELIGSAMGLNEQPVLVNVNRPARRAGNADELIGNAMGLNEQPVLVNVNRPARRAGNA
| | | | |
g225      NADELIG-----GAMGLNEQPVVVRVNRAXARRAGNA
                                70      80      90

      120     130     140     150     160     170
m225.pep  DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
| : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | : | | |
g225      DKLIGSAMRLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100      110      120      130      140      150

      180     190     200     210     220     230
m225.pep  SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g225      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
              160      170      180      190      200      210

      240     249
m225.pep  VKKNDPSRFLNX
| | | | |
g225      VKKNDPSRFLN
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

a225.seq

```
1 ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51 TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCTGGCG GCGGGCGGGG AATGCCGAGC AACTCATCGG
201 CAGCGCGATG GCGCTTAAAG AACAGCCCGT TTACCGCTGC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGGG CAATGCCGAC
451 GAACTCATCG GCAACCGGAT GGGACTTTTG GGTATTGCCT ACCGTCACGG
501 CGGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA
```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

a225.pcp

1	MDSFFKPAVW	AVLWLMFAVR	PALADELTLN	LSSREQILRQ	FAEDEQPVLP
51	INRXPARRAG	NADELIGSAM	GLNEQPVLPV	NRXPARRANG	ADXLIGNAMG
101	LNEQPVLPVN	RVPARRAGNA	DELIGNAMGL	NEQVLPVNR	APARRAGNAD
151	ELIGNAMGGL	GIAYRYGGTS	ISTGFDCSGF	MQHIFKRAMG	INLPRTSAEQ
201	ARMGTPVAR	ELQPGDMVXF	RTLGGSRISH	VGLYIGNNRF	IHPARTGKNI
251	EITSLSHKYW	SGKYAFARRV	KKNDSPRFLN	*	

m225/a225 87.4% identity in 277 aa overlap

```

                                10      20      30      40      50
m225.pep      FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
                | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a225          MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPAR
                10      20      30      40      50      60

                                60      70      79      80
m225.pep      NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA

```

```

a225      |||||
          NADELIGSAMGLNEQPVLFPVNRXPARRAGNADXLIGNAMGLNEQPVLFPVNRVPARRAGNA
          70      80      90      100      110      120

m225.pep  90      100      110      120      130      140
          DELIGNAMGLNEQPVLFPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
          |||||

a225      130      140      150      160      170      180
          DELIGNAMGLNEQPVLFPVNRAPARRAGNADDELIGNAMGLLGIAYRYGGTSISTGFDCSGF

m225.pep  150      160      170      180      190      200
          MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||||

a225      190      200      210      220      230      240
          MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFXFRTLGGSRISHVGLYIGNNRF

m225.pep  210      220      230      240      249
          IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
          |||||

a225      250      260      270      280
          IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg cgcacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttacct
151  gtcaaccgag ccccgcccg ggcggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251  cgcgccggcg ggcgggcaat gccgacaaac tcacgcggag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggtt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcg cacgtcggcg gaacaggcgc ggatgggcgc acccgttgcc
451  cgaagcgaaat tgcagcccg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcgcgcg cagggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgccgc cgggtcaaga aaaacgacct
651  gtcacgcctt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LGLIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCGGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTGCCCAGAG ACGAACAGCC CGTTTTACCC
151  ATCAACCGAG CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCGCGG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCCGTTT ACCCGTCAAC CGAGCCCCCG CCCGGCGGGC
351  GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGT TTCCGCACGC TCGGCGGCAG CCGCATTTC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCCGG GTCAAGAAAA ACGACCCGTC CCGCTTTCTG
751  AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

          10      20      30      40      50      60
m225-1.pep MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
          |||
g225-1      MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
          10      20      30      40      50      60

          70      80      90      100     110     120
m225-1.pep NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
          |||
g225-1      NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
                      70      80      90

          130     140     150     160     170     180
m225-1.pep DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
          |||
g225-1      DKLIGSAMRLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
          100     110     120     130     140     150

          190     200     210     220     230     240
m225-1.pep SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
          |||
g225-1      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
          160     170     180     190     200     210

          250
m225-1.pep VKKNDPSRFLNX
          |||
g225-1      VKKNDPSRFLNX
          220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCGCCCGCCC GCGGGCGGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCC T ACCGTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGA CTG CAGCGGCTT ATGCAGACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCCG
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRFI IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDDPSRFLN *

```

a225-1/m225-1 88.6% identity in 280 aa overlap

	10	20	30	40	50	60
a225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG					
m225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a225-1.pep	NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA					
m225-1	NADELIGSAMGLNEQ-----VLEPVNRVPARRAGNA					
	70				80	90
	130	140	150	160	170	180
a225-1.pep	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF					
m225-1	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF					
	100	110	120	130	140	150
	190	200	210	220	230	240
a225-1.pep	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF					
m225-1	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF					
	160	170	180	190	200	210
	250	260	270	280		
a225-1.pep	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDRPSRFLNX					
m225-1	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDRPSRFLNX					
	220	230	240	250		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101  GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151  CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201  TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251  GCCGTAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC GCAGCTTGCG
301  GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351  gccggatacc caattctcct tccgcctcgt tcttcaatat ctgttattta
401  caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451  tttctgttgc ctccgcctct cctgccgcgc ctcggcccgcc atacattcgg
501  ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551  cagttgtggt cctttctcct Ccgggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLSV TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
101  GSVTGIVTGM YFAAWLGPDT QFSFPRLQY LLFTPSGIPI HTLYARVLPP
151  FLLPPPLLPR LGPHTLRRFT ILPKKLRFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGTACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101  GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151  CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201  TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251  GCCGTAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC ACAGCTTGCG
301  GGCAGCGTTA CGGCATTGT TACAGGATG TATTTTGCCA AATGGCTGGG
351  CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401  CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451  GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGTATGGCGG CATAACGCGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep
 1 MNEILROPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIIVTGM YFAKWLGAER EVVLSLASKS VTNPPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

m226.pep	10	20	30	40	50	60
	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
m226.pep	70	80	90	100	110	120
	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
m226.pep	130	140	150	160	170	180
	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
g226	QFSFPPRLOYLLFTPSGIPHTLYARVLPFPFLPPLPRLGPHTLRRFTILPKKLRFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq
 1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
 51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
 251 GCCGTAAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGGC
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGCATGGCGG CATAACGCGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep
 1 MNEILROPSI LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA
 101 GSVTGIIVTGM YFAKWLGAER EVVLSLASKS VTNPPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60


```

m226.pep  MNEILRQPSVLLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
a226      MNEILRQPSILLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
           10      20      30      40      50      60

           70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
a226      AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
           70      80      90      100     110     120

           130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVSG
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVSG
           130     140     150     160     170     180

           190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
a226      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgcggg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccgcc agcatcgctg
101 gcatgggcgt gctgtttgcg cttttgcagg cgggttggt caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttcct
201 cgtgccgccc tgcgtggcgg tcatcagcta ttgggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaagggtca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1  MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLF LLQAGWLKTS
51  WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWF SILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1  ..ACGTCTTkgC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTTG GATTTGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1  ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

           10      20      30
m227.pep  TSXLQQLTDALMSNLTFLVPPCVAVISYL
           || |||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTLFLVPPCVAVISYL
           20      30      40      50      60      70

           40      50      60

```

516

```

m227.pep  DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
          |||||||||||||||||||||||||||||
g227      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
          80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTTCG CTTTTCGAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCG TGCCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGGTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGTTTACAG GCAAGTTCA CCGCTGGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLOAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep                                     10      20      30
                                         TSXLQQLTDALMSNLTFLVPPCVAVISYL
a227                                     || |||||:|||||
TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
20      30      40      50      60      70

m227.pep          40      50      60
          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
          |||||||||||||||||||||||||
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
          80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

a228.pep
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
 101 KMKDAAK*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq
 1 atggctgccc tatcggggcgg cggcgccggtc ttccctgataa tgcttccaca
 51 tattgcccgc gtccagcgtc agccgccagc gtccgcccga gcgtcgggag
 101 aaatcgccat tgaagccgcc ggcgaaattg tatcgggtgc cgcccaagag
 151 gttttgccc acaaacggca cggcgccgaa cgagcgcggt accgaacggt
 201 tttgatggcc gaacgacagg cgcaggttct gtccgctgaa atctttgtta
 251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgccc
 301 gcccgcattg atttcgcgcg acacgcccga gccgtagcgc aaaccgtgtg
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
 401 tcaatcgttt tttcggacga agcgttggtt atagcggatt aacaaaaatc
 451 aggacaaggc ggcggggccgc aggcagtacg gatggtacgg aaccggttcg
 501 cccggtgctt ggacgcctta gggaaccgtt ccctttgagc cggggcgggg
 551 caaccggtac cgggttttgt tcatccgccca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep
 1 MAAVSGGGAV FLIMLPHIAR VQROPFAFAQ ASGEIGIEAA GEIVSAAAOE
 51 VLPDKRHGAE RARYRTVLM AERQAQVFAE IFVIPIMHAA ADAAVEEMMP
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTGI
 151 RTRRRAAGST DGTEPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
 251 CCCTAGCGCA AACCGTGTGC CTTTTCGCGC AGGCTGTCGG CGGTTTTCGT
 301 CCAGCTTCTG CCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTTTA
 351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
 401 AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACcTTA GAGAATCGTT
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)
 1 ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
 51 AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTVC LLRQAVGGFR
 101 PASARKFNRF FGRSVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
 151 SLFCSSAILC *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      MAAVSGGGAVFLIMLPHIARVQRPPAFAQASGEIGIEAAGEIVSAAAEVLPDKRHGAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIFVPIPMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RARYRTVLMARQAQVLF AEI FVPIPMHAAA -DA AVEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRE----
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRRAAGSTDGTEPVRPVLGRLREPFPL
                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSLFCSSAILCX
                :|: ||| ||| ||| |||
g229      SRGGATRTGFCSSAILC
                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

```

a229.seq (partial)
1  ATGGCTGTCG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCAC GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCGCTGATG TCTCCGTAGA GGAATGATG
301 CCCGCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTCAATCG TTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTCAGCACC TTAGAGAATC GTCTCTTTGA GCTAAGGCGA
551 GGCAACGCCG TACTGGTTT TGTTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

```

a229.pep (partial)
1  MAVVSGGGAV FLITLPHIAH VQRPPXFAQ ASGEIGIEAA DEIVSAAAE*E
51  VLLDKRHDAE *ARY*TVFIA EROAQALFAE IFVILIVHAA AADVSEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRRFG RSVVYSGLTG
151 ITRRRSADS TDSTEPINLV LQHLRESSL* AKARQRRGTG CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      MAVVSGGGAVFLITLPHIAHVQRPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIFVPIPMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      XARYXTVFIAERQAQALFAEIFVILIVHAAAADVSVEEMMPARIDFARHAQAVAQTVCLL
                70      80      90      100     110     120

```

```

              100      110      120      130      140      149
m229.pep      RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---
              |||||
a229          RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX
              130      140      150      160      170      180

              150      160
m229.pep      -----RSLFCSSAILCX
              |: |||:|
a229          AKARQRRTGFCSSSTI
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```
g230.seq
1 atgttccatt ccatcgaaaa atacagaaca cccgcccaag tcttattagg
51 cctgattgca ttaacttttg tgggtctcgg cgtcagcacg gtttcccatc
101 cgggcgcgca ctacatcgtc caagtgggcg acgaaaaaat cagcgcagcac
151 tcaatcaaca acgcatcgca gaacgagcag gcgcgacggc gcagcccttg
201 gcgcgacgcy gttgtccaat ccctgctgca acgcgccttac ctgaaacattg
251 gcgcgaagct gatgggcatt tgggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtacgcg
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtttg
401 tcgaagaaat ccgcgatcag tttgccttgc agaattttgtt aagcctcgtc
451 caaacggcg ttttggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgcccc agtcaaagcg tctgaagccg atttgagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaa attggaatatgt
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag cgcgttgccg acttcaacaa ggcaaaaaga aagctgggcy
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaaccca agaaaacttg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaaa acctaataa tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaa tccgaagtgc tgaccatcaa cagcgaaacc
1051 cgtggggtcg tccgcgccaa agaagtcggc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatcggg tgcgtcaggc ctatatccgt accgaagccg
1151 caaaactttt gaaaacaatg taa
```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

g230.pap

1	<u>MFHSIEKYRT</u>	<u>PAQVLLGLIA</u>	<u>LTFVGFVST</u>	<u>VSHPGADYIV</u>	<u>QVGDEKISEH</u>
51	SINNAMQNEQ	ADGGSPWRDA	VFQSLQRAY	LKQGAQLMGI	SVSSEQIKQM
101	IVDDPNFHDA	NGKFSHALLS	QYLSQRHMSE	DQFVEEIRDQ	FALQNLVSLV
151	QNGVLVGDAQ	AEQLIRLTQV	NRTIRSHTFN	PDEFIAQVKA	SEADLQKFYN
201	ANKKDYLLPQ	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPAHE
251	AKPSFEQEKA	AVENELMKKK	AVADFNKAKE	KLGDADFNNHP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG	MPENLINAVF	SDDVLKKKHN	SEVLTTINSET
351	AWVVRAKEVR	EEKNLLFEEA	KDAVROAYIR	TEAAKLLKTM	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```
m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCGTATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAaT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCc.GACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAT CAAGCAAATT
301 ATCGTGAGCG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
```

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTCGAAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSDA VFQSLQRAY LKQGAklMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGD DAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKTL PFAEA KDAVRQAYIR TEAAKL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

```

m230/g230
      10      20      30      40      50      60
m230.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
          |||||
g230      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
          |||||

      70      80      90      100     110     120
m230.pep ADGGGSPSDAVFQSLQRAYLKQGAklMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN
          |||||
g230      ADGGSPWRDAVFQSLQRAYLKQGAklMGISVSSEQIKQMI VDDPNFHDANGKFSHALLS
          |||||

      70      80      90      100     110     120

      130     140     150     160     170     180
m230.pep RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          :|||
g230      QYLSQRHMSDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          |||||

      130     140     150     160     170     180

      190     200     210     220     230     240
m230.pep PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          |||||
g230      PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          |||||

      190     200     210     220     230     240

      250     260     270     280     290     300
m230.pep ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAVNHP SSLAEAAKNS
          |||||
g230      ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGD DAFNHP SSLAEAAKNS
          |||||

      250     260     270     280     290     300

```

521

	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPPFAEAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCGCCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	CTACATCGTC	CAAGTGGGCG	ACGAAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	GCGGACGGCG	GCGGCCCTTC
201	GCGCGACGCG	GTGTTCCAAT	CCCTGCTACA	ACGCGCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	AACGGCAAAT	TCGACCACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGTCTGAA	GACCAAGTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCCTTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG	CGACGCGCAG	GCGGAACAGC	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCCGTTTCGA	CACCTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCTGAAGCCG	ATTTGCAGAA	GTTTTATAAC
601	GCAAACAAA	AAGACTACCT	GCTTCCCAA	GCGGTCAAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTGCAGACAA	ACAGACCGTC	AGCGAAACAG
701	AAGTGAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAAATGAA
751	GCCAAACCTT	CTTTCGAGCA	GGAAAAAGCC	GCCGTCGAAA	ACGAATTGAA
801	AATGAAAAAG	GCGGTTGCCG	ACTTCAATAA	GGCAAAGAA	AAGCTGGGCG
851	ATGACGCGTT	CAACCATCCT	TCCTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAAG	TCGAAACCCA	AGAAACTTGG	CTGAGCAGGC	AGGATCGCGA
951	AATGTCCGGT	ATGCCCGAAA	ACCTGATCAA	TGCCGTATTC	AGCGACGACG
1001	TATTGAAGAA	AAAACACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTCG	TCCGCGCCAA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTT				

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

1	MFHSIEKYRT	PAQVLLGLIA	LTFVGFVST	VSHPGADYIV	QVGDEKISDH
51	SINNAIQNEQ	ADGGGSPSRDA	VFQSLQRAY	LKQGAALMGI	SVSSEQIKOI
101	IVDDPNFHDA	NGKFDHALLN	RYLSQRHMSE	DQFVEEIRDQ	FALQNLVNLV
151	QNGVLVGDAQ	AEQLIRLTQV	NRTIRSHTFN	PDEFIAQVKV	SEADLQKFYN
201	ANKKDYLLPK	AVKLEYVALN	LKDFADKQTV	SETEVKNAFE	ERVARLPANE
251	AKPSFEQEKA	AVENELKMKK	AVADFNKAKE	KLGDDAFNHP	SSLAEAAKNS
301	GLKVETQETW	LSRQDAQMSG	MPENLINAVF	SDDVLKKKHN	SEVLTINSET
351	AWVVRakeVR	EEKTLPPFAEA	KDAVRQAYIR	TEAAKL	

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPSPDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
a230	ADGGGSPSRDAVFQSLQRAYLKQGAALMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

m230.pep	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRL	TQVNR	TIRSH	TFTN
a230	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRL	TQVNR	TIRSH	TFTN
	130	140	150	160	170	180			
m230.pep	PDEFIAQVK	VSEADLQ	KFYNNKK	DYLLPQAV	KLEYVALN	LKDFADK	QTVSE	TEVKNA	FE
a230	PDEFIAQVK	VSEADLQ	KFYNNKK	DYLLPQAV	KLEYVALN	LKDFADK	QTVSE	TEVKNA	FE
	190	200	210	220	230	240			
m230.pep	ERVARLPAN	EAKPSFE	QEKAAVE	NELKMKK	AVADFNK	AKEKLGD	DAVNHP	SSLAE	AAKNS
a230	ERVARLPAN	EAKPSFE	QEKAAVE	NELKMKK	AVADFNK	AKEKLGD	DAVNHP	SSLAE	AAKNS
	250	260	270	280	290	300			
m230.pep	GLKVETQET	WLSRQDA	QMSGMP	ENLINAV	FSDDVLK	KKHNSE	VLTI	INSETA	WVVR
a230	GLKVETQET	WLSRQDA	QMSGMP	ENLINAV	FSDDVLK	KKHNSE	VLTI	INSETA	WVVR
	310	320	330	340	350	360			
m230.pep	EECTLPFAE	AKDAVRQ	AYIRTEA	AKL					
a230	EECTLPFAE	AKDAVRQ	AYIRTEA	AKL					
	370	380							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCTCATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATGTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTGCA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAGAAAGC GCGGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCCG CAAAACAGC
901 GGTTTGAAAG TGGAACCCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TGCGTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CGAAAACAAG GCAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCGA TTGACGTGAA ATGGTCGGAA GTGTCGGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGGC AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCTGCCG
1351 GCACCCGTA TTGTCGAGGC GCAGGCAGTC ACGCTCCCG AGGATATTGC
1401 CGCACAGCTT CCTCTGCGA AACAGGCTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGCTGATC CGCTATTTCA ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEKIQM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHME DQFVEEIRDQ FALQNLVSLV

```



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151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWSE VSVLGAQQAQ QSMPPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGCGC ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGCTGTA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGA CACTTTCAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 CGGAACAAAA AAGATATCT GCTGCCGAG GCGGTCAAAT TGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCAATTTGAA GAGCGCGTGG CCGGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCGGTATTG AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGCG
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGC CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCGCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTTGA CTGTTGATA CGTTATTTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAklmgi SVSSEIQIKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWVVRakeVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWSE VSVLGAQQAQ QSMPPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230-1.pep	ADGGGSPSRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQGAklmgiSVSSEIQIKMIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m230-1.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRNRTIRSHTFN					

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 837>:

1	ATGTTCCATT	CCATCGAAAA	ATACAGAAGC	CCGCCCCAAG	TCCTTTTGGG
51	CCGTGATTGA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTCCCGA	CTACATCGTC	CAAGTGGCGG	ACGAAAAAAT	CAGCGACCAT
151	TCCATCAACA	ACGCCATACA	GACGAACAGC	CGGGACCGCG	CGGGCCCTTC
201	GCGCGACGCG	GTGTTCCAAT	CCCTGCTACA	ACGCGCCTAC	CTGAAACAGG
251	GCGCGAAGCT	GATGGGCATT	TCGGTTTCCT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGAGC	ATCCCAAATT	CACGACGACA	AACGGCAAAAT	TCGACCACGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGTCTGAA	GACCAAGTTG
401	TCGAAGAAAT	CCGCGATCAG	TTTGCTTTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGCGC	TATTGTCGCG	CGACGCGCAG	CAGGAAACAG	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCGGTTGCBA	CCTTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCGGAAGCCG	ATTTGCAGAA	GTTTTATAAC
601	GCAAAACAAA	AAGACTACCT	TGCTCCCAAA	GCGGTCAAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TGTCAGACAA	ACAGACCGTC	AGCGAAACAG
701	AACTGAAAAA	TGCGTTTGAA	GAGCGCGTGG	CGCGTTTGCC	GGCAAAATGAA
751	GCCAAACCTT	CTTTTCGACA	GGAAAAAGCC	GCCGTCGAAA	ACGAAATGAA
801	AATGAAAAAG	GCGGTTGCGC	ACTTCAATAA	GCGAAAGAA	AAAGCTGGGC
851	ATGACGCGTT	CAACCATCCT	TCCTCGCTTG	CCGAAGCCGC	CAAAAACAGC
901	GGTTTGAAG	TCGAAACCCA	AGAAATCTGG	CTGAGCAGGC	AGGATCGCA
951	AATGTCGGT	ATGCCCGGAA	ACCTGATCAA	TGCCGTATT	AGCGACGACG
1001	TATTGAAGAA	AAAACACAAT	TCGGAATGTC	TGACCATCAA	CAGCGAAACC
1051	GCGTGGGTCG	TCCGCGCCAA	AGAAGTCCGC	GAAGAGAAAA	CCCTGCCGTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTCAGGC	TTATATCCCT	ACCGAAGCCG
1151	CCAAACTTGC	GAAAAACAAG	GCAAAAGAGC	TGCTTACCGA	ACTGAACCGC
1201	GGCAAGGCTG	TTGACGTAAG	ATGGTCGGAA	GTGTCGGTTT	TGGGCGCACA
1251	CGAGGCAAGG	CAGTCAATGC	CGCCCCGAGC	TTATTCGGAA	CTGCTGAAAG
1301	CAAAACCGCG	AAACCGCAAA	CCCCCTACG	TCAGGCTGAT	CGGTCTGCCG
1351	GCACCCGTGA	TTGTGCAAGT	ACAGGCTGTA	ACCCCGCCGG	ATGATATCGC
1401	CGCACAGCTT	CCGCTTGCAA	AACAGCTTTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTCCA	CTTGTTGATA	CGTTATTCTA	ACGGCAAAAT	CAAACAGACC
1501	AAAGGAGCGC	AATCGTTCGA	CAACGCGCAC	GGTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKTLFFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLNG
401 GKAVDVKWSE VSVLGAQQAQ QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

1	atgtcaaaac	gaaaaatccat	aaaccgtcgc	tatcaaaaaac	cggcggaact
51	gccgcgcttg	caaaaataatc	cgccatttta	ccgtaaaaaac	cgccgcctga
101	acttttttat	cgcgcgcagac	ggcgggtgcg	cgtctccgca	aaaatgcagg
151	gcgcgcgggt	ttcagacggc	atttgccgtt	caaggccgtg	cggtgtcttt
201	accaaatgcc	caaccattcg	cccacggaat	ccatccaatc	cttattgccc
251	ccgcgcctcc	tgctgcgccg	cggttagcgc	cacggcgctt	gcgagttttt
301	agctttccac	aatcctttgc	gttccctttc	cgcctgaatt	tggcgcctcg
351	catagtcggc	aaaatccgcc	ttatcctgct	gttcttttagc	ataactttta
401	taatgccacg	ccgccccgctc	ctgcacctgc	atcagggttca	aatcggtttt
451	gcgggcggat	acctgcgcca	cttcgcgctg	atagcggtcg	gtttcaaaca
501	cacgtacact	gactttccta	ccctccgcgc	ccgcgcgcag	gttgtcgcgc
551	gaacgtgtac	cgtaaagctg	tttcatcttc	ggtgcgctga	tatacgccat
601	ccgaatttta	tgtttcgcgc	cgtcgcgcgc	gatcacgtga	agggatctcg
651	cgtcatagac	tttggacacc	gtgcctgtgt	agctgtggcc	ggatttcgcc
701	gatgcccgctc	ggcgaacggg	cgcgtcgaaa	cccacgtccc	ctgcagtgcc
751	gagtacgtcg	agtacggcaa	ccgccgtccg	caccgcctca	ctgtcatatc
801	ccgtataacc	caacgcgccc	aaaagcgaca	gggcgcacggg	aagccatttc
851	atgatttttt	taatctgcat	atttttcaaa	tgccgatgcc	gtctgaacat
901	ctctga				

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

1	MSKRKSINRP	YQKPAELPPL	QNNPPFYRKN	RRLNFFIAAD	GGCASPQKCR
51	ARGFQTAFAV	QGRAVSLPNA	QFFAHGIHPI	LIAPAAPACP	AVRPRRLRIF
101	SFPQSFAFPF	RLNLSVGIVG	<u>KIRLILLFFS</u>	<u>ITFIMPRRPV</u>	LHLHQVQIGF
151	AGGYLRHFAL	IAVGFKHTYT	DFPTLRRRAQ	VVARTCTVSL	FHLRCVDIRH
201	PNFMFRAVAV	DDVKGIAVID	FGHRACVAVA	GFRRCPSANG	RVETHVPCSA
251	EYVEYGNRRP	HRLTVISRIT	QRAQKROGDG	KPFHDFFNLH	IFQMPMPSEH
301	L*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

1	ATGTCAAAAC	GAAATCCAT	AAACCGTCCG	TATCAAAAAC	CGCGGAACT
51	GCCGCCGTTG	CAAAATAATC	CGCATTTTA	CCGTAAAAAC	CGCCGCCTGA
101	ACTTTTTTAT	CGCGGCAGAC	GGCGGTTGCG	CGTCTCCGCA	AAAATGCAGG
151	GCGCAAGCGT	TTACAGCGGC	ATTTGCCGTT	CAAAGCCGTG	CGGTGTCCTT
201	ACCAATGCC	CACCAATTCG	GC....		

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRAVSLPNA QPFG.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng)

from *N. gonorrhoeae*:

```

                10      20      30      40      50      60
m231.pep      MSKRKSINRPYQKPAELPPLQNNPPFYRKNNRLNFFIAADGGCASPQKCRARGFQTAFV
                |||||
g231          MSKRKSINRPYQKPAELPPLQNNPPFYRKNNRLNFFIAADGGCASPQKCRARGFQTAFV
                10      20      30      40      50      60

                70
m231.pep      QSRVSLPNAQPFQ
                |:|||||:
g231          QGRAVSLPNAQPFQAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFRLNLSVGIVG
                70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

a231.seq (partial)

```

1  ATGTCAAAAC  GAAAATCCAT  AAACCGTCCG  TATCAAAAC  CGGCGGAAC
51  GCCGCCGTTG  CAAAATAATC  CGCCATTTTA  CCGTAAAAAC  CGCCGCCTGA
101 ACTTTTTTAT  CGNGGCAGAC  GCGGTTGCG  CGTCTCCGCA  AAAATGCAGG
151 GCGCGCGGTT  TTCAGACGGC  ATTTGCCGTT  CAAAGCCGTG  CCGTGTCTTT
201 ACCAAATGCC  CAACCATTCT  CCCACGGCAT  CCATCCAATC  CTTATTGCCC
251 CCGCCGCTCC  TGCCTGCCCG  GCGGTACGCC  CACGGCGCTT  GCGGATTTT
301 AGCTTTCCAC  AATCCTTTGC  GTTCCCTTTC  CGCCTGAATT  TGAGCGTCGG
351 CATAATCGGC  AAAATCCGCC  TTATCCTGCT  GTTCTTTAGC  ATAACTTT
401 TAATGCCACG  CCGCCCCGTC  CTGCACCTGC  ATCAGGTTCA  AATCGGTTTT
451 GCCGACAGAA  ACCTGCGCCA  CTTCGCGCTG  GTAGCGGTCG  GTGTGGAACA
501 CGCGGACGCT  GACTTTCTCT  CCTCCGCCG  CCGCGCGCAG  GTTGTGCGCG
551 GAACGCGTGC  CGTAAGCCTG  TTTCATCTCC  GGCGCGTCGA  TATACGCCAT
601 CCGGATTTTG  TGTTCGCGC  CGTCGCGCTC  GATAACGTGA  AGGGTGTGCG
651 CGTCATAGAC  TTTGGACACC  GTGCCTGTGT  AGCGGTGGCC  GGATTTCGCC
701 GATGCTCGGC  GCGGGGCGGG  CGCGTCGGAA  CCCGCGTCCC  CTGCCGCGCC
751 GAGTACGTCG  AGTACGGCAA  CCGCCGTCG  CACCGCCTCG  CTGCCGTACC
801 CCGTATAACC  CAACGCACCC  AAAAGCGACA  AGGCGACGGG  AAGCCATTTT
851 ATGATTTTTT  TAATCTGCAT  ATTTTTCAAA  TGCCGATGCC  GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1  MSKRKSINRP  YQKPAELPPL  QNNPPFYRKN  RRLNFFIXAD  GGCASPQKCR
51  ARGFQTAFV  QSRVSLPNA  QPFAHGIHPI  LIAPAAPACP  AVRPRRLRIF
101 SFPQSFAFPF  RLNLVGIIG  KIRLILFFS  ITFIMPRRPV  LHLHQVQIGF
151 ADRNLRHFAL  VAVGVEHADA  DFPAFRRRAQ  VVARTRAVSL  FHLRRVDIRH
201 PDFVFRAVAV  DNVKGVAVID  FGHRACVAVA  GFRRCSAAGG  RVGTRVPCRA
251 EYVEYGNRRP  HRLAAVPRIT  QRTQKRQGDG  KPFHDFEFLH  IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFQ					
a231	QSRVSLPNAQPFQ					
	70	80	90	100	110	120
	QSRVSLPNAQPFQAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIIG					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1  ATGTCAAAAC  GAAAATCCAT  AAACCGTCCG  TATCAAAAC  CGGCGGAAC
51  GCCGCCGTTG  CAAAATAATC  CGCCATTTTA  CCGTAAAAAC  CGCCGCCTGA
101 ACTTTTTTAT  CGCGGCAGAC  GCGGTTGCG  CGTCTCCGCA  AAAATGCAGG
151 GCGCGCGGTT  TTCAGACGGC  ATTTGCCGTT  CAAGCCGTG  CCGTGTCTTT
201 ACCAAATGCC  CAACCATTCT  CCCACGGAAT  CCATCCAATC  CTTATTGCCC
251 CCGCCGCTCC  TGCCTGCCCG  GCGGTACGCC  CACGGCGCTT  GCGGATTTT
301 AGCTTTCCAC  AATCCTTTGC  GTTCCCTTTC  CGCCTGAATT  TGAGCGTCGG
351 CATAGTCGGC  AAAATCCGCC  TTATCCTGCT  GTTCTTTAGC  ATAACTTT
401 TAATGCCACG  CCGCCCCGTC  CTGCACCTGC  ATCAGGTTCA  AATCGGTTTT
451 GCCGGCGGAT  ACCTGCGCCA  CTTCGCGCTG  ATAGCGGTCG  GTTCAAAcA
501 CaCgTaCaat  gagtttcgta  ccctccGCGG  ccgcgcgCAG  GTTgtcgcGC
551 GAACgTGtAC  CGTAagcgtg  Ttcatctcc  GGTGcgtcGA  TATACGCCaT
601 cCgAATTtta  tGtttcgcgc  cgtcgcCgtc  gATGACGTGA  AGGgtatcGC
651 CgtcATAGAC  TTTGGACACC  Gtgctgcgt  AGctGTGGCC  GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1  MSKRKSINRP  YQKPAELPPL  QNNPPFYRKN  RRLNFFIXAD  GGCASPQKCR
51  ARGFQTAFV  QSRVSLPNA  QPFAHGIHPI  LIAPAAPACP  AVRPRRLRIF

```

101 SFPOSFAFFP RLNLVGIIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH
201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

```
1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTAA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTC AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTATCGAACA
501 CCGGCACGCT GACTTTCCTG CTTCCGCGC CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGCGGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

```
1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
101 SFPOSFAFFP RLNLVGIIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLRHFAF VAVGIEHAHA DFPFERRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIQFQTAS*
```

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPOSFAFFPRLNLVGIIVG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFPOSFAFFPRLNLVGIIVG					
	70	80	90	100	110	120
g231-1.pep	KIRLILLFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRLRHFAFVAVGIEHAHADFPFERRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIIVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAVIDFGHRACVAVAGFRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

```
1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGGTTGCG CGTCTCCGCA AAAATGCAGG
```

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151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCGGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGGAACA
501 CCGGACGCT GACTTTCCTG CCTTCCGCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGTCTGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTGCGC
701 GATGCTCGGC GCGGGGCGGG CCGCTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAV VAVGVEHADA DFPFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIIG
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFPQSFAFPFRLNLVGIIG
a231-1.pep	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGVEHADADFPFRRAQ
m231-1	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHADADFPFRRAQ
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAIDFGHRACVAVAGFRCSAAGG
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAIDFGHRACVAVAGFRCSAAGG
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH
a231-1.pep	IGIGFQTASX
m231-1	IGIGFQTASX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgctt tatattgtcg
101 ggatactggt ttgtctggtc gccgtcggag gaacggccgg cagcctgttt

```

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtgggaatat
201 tgtccgtggg acaaaatccc tgctgcgtga aacgggtcgg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggg tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgccgccc
401 gttcgggtact gtgtgccaag ttcggcaggg aacgggtgat gttggcttgg
451 gtaacgggtt gtgcgttggg ttcgacgggt tgcggcctgg ttttggtgtg
501 gctgacgcac ggacaccggt ttgaaggggt gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cgggtgatgac gctgatcggc
601 tttttcggcg gattttttctc cgttccgctc tatacctggc tgcaaaccgc
651 cagcagcgag actttccgcg cccgcgcggt tgcgcgcaac aatatcgtaa
701 acggcatctt tatggtttcc gccgcggtt tgagcgcggt attgctgttt
751 ttgtttgaca gcatttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgcg aaggcggttt ttaggcgcgg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLIRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VELIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCTGTGT
51 CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCT TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC ACAAATCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCCG
251 TTTTACC GC CATTATCGGT ATTTCTGTGT TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTC AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TCGCGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCGGC
601 TTTTTCGCGC GATTTTCTC CGTTCGCTC TATACCT(g)TG CAAACCGCCA
651 TAGCGAGaTT TCCGCGCCCG GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGG TTTCCGCTGC CGTTTTGAGC GCGGTGTTGC TGTTTTGTG
751 TGACAGCATT TCCTTGTGT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTATAG CGCGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLIRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

          10          20          30          40          50          60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||||
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```


531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232 . pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	130	140	150	160	170	180
m232 . pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFSRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	190	200	210	220	230	
m232 . pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAANAANNIVNGIFMVS					
	240	250	260	270	280	289
m232 . pep	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPAVFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232 . seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTC
101 AAACCGCGCT GTTTGTGATG ATTGGGTTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAACCTG GGCGCGTTGC TGTATTATTT
201 GCCGTATTC CTGTTTTTCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCGCG TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTGTGCGCC ATCCTGTTCC GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGGTCCG CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT CCGCTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGGAAATATT TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTCC GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTTT CCATCGGTAT TGCCGCGGCT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGAA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CGGCTTGGTT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCGGCGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTAA
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTCGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTATT AAGCGCGAAA GCGGTTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232 . pep
1  MYAKKGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLLACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFVA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPVS
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNML ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLEFLDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILEDYLDDELMMGNSLIESGTFVAILFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232	YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG						
	180	190	200	210	220	230	
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSXERLMLAW					
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSRERLRLAW						
	240	250	260	270	280	290	
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
a232	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL						
	300	310	320	330	340	350	
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232	YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS						
	360	370	380	390	400	410	
m232.pep		270	280	289			
		VFLIKRERRFLGAAAIRKKPX					
a232	VFLIKRERRFLGAAAIRKKPX						
	420	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

1	atgaaacgca	aaaatatcgc	gctgattccc	gccgccggca	tcgggggtgcg
51	tttcggtgcg	gacaaaccca	agcaatatgt	cgaaatcgga	agcaaaaccg
101	ttttagaaca	tgtacttggg	atTTTTgaac	ggcatgaggc	cgtcgatttg
151	accgtcgttg	tcgtctcgcc	cgaagacacg	tttgccgata	aggttcagac
201	ggcatttcca	caggttcggg	tgtggaaaaa	cggtggacag	acccgcgcgcg
251	aaactgtccg	caacggtgtg	gcaaaactgt	tggaaaccgg	tttggcggcg
301	gaaaccgaca	atattctggt	acacgatgcc	gcccgctgct	gcctgccgtc
351	tgaagctctg	gcgcggttga	tagaacaggc	gggcaacgcc	gccgaaggcg
401	ggattttggc	agttcccgtt	gccgatacgc	tcaagcgcgc	agaaagcgga
451	caaatacgtg	caactgtcga	cgttccgggg	ctttggcagg	cgcaaacgcc
501	gcagcttttt	caagcgggtt	tgctgcaccg	cgcattggct	gcggaaaact
551	tgggcggcat	taccgatgaa	gcgtccgcgc	tggaaaaact	gggtgtgcgt
601	ccgctactga	tacagggcga	cgcgcgcaat	tgaaactga	cgcagccgca
651	ggacgcatac	atcgtcaggc	tgctgctcaa	tgccgtctga	

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

1	<u>MKRKNIALIP</u>	<u>AAGIGVRFGA</u>	<u>DKPKQYVEIG</u>	<u>SKTVLEHVLG</u>	<u>IFERHEAVDL</u>
51	<u>TVVVVSPEDT</u>	<u>FADKVQTAFP</u>	<u>QVRVWKNNGQ</u>	<u>TRAETVRNGV</u>	<u>AKLLETGLAA</u>
101	<u>ETDNILVHDA</u>	<u>ARCCLPSEAL</u>	<u>ARLIEQAGNA</u>	<u>AEGGILAVPV</u>	<u>ADTLKRAESG</u>

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
 201 PLLIQGDARN LKLTQPDAY IVRLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCCA CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG
 401 GGATTTTGGC AATTCCCAT TCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
 101 ETDNILVHDA ARCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	: : : : :					
g233	MKRKNIALIP AAGIGVRFGADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	: : : : :					
g233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
	: : : : :					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC
 201 GGCATTTCCA CAGGTTCTGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG
 251 AAACGTGTCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATTCCCGTT GCCGATACGC TCAAGTGCGC GGACGGTGGG
 451 AACATTAGTG CAACCGTCGA CGGACGAGC CTTTGGCAGG CGCAAACGCC
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAACT
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPDQDAY IVRLLLDAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

10      20      30      40      50      60
m233.pep MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
|||||
a233      MKRKNIALIPAAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
10      20      30      40      50      60

70      80      90      100     110     120
m233.pep FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
|||||
a233      FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
70      80      90      100     110     120

130     140     150
m233.pep TRLIEQAGNA AEGGILAIPIADTLKCADGGNI
|||||
a233      TRLIEQAGNA AEGGILAIPIADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPDQDAYIVRLLLDAVX
190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgcgcg catcgctttt gccgcgcgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cagggtgttc gcaccccgat ttccgctcga
151 acattcgaca accgctccag cttccaaaaa ggcattttct cgcacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca caccgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaaatccg gcatttcccg caaagcgag aacctgaaag gcgcagatta
351 tgtcgttacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccgggtac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcatggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSOAKTILVT HLQQTNRNFV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGGTSY DATLNGKVLD
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGt GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gtCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

					10	20	30
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL		
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQGAGEYALSNREIIGFGGTSGYDATLNGKVL						
	140	150	160	170	180	190	

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
	:		
g234	DLAIREAVDNLVQAVDNGAWQSNRX		
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCOA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG*
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD*
 101 ATLNGKVLDL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

					10	20
30						
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL	
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQGAAGEYALSNREIIGFGGTSGYDATLNGKVL					
	50	60	70	80	90	100

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
a234	DLAIREAVNSLVQAVDNGAWQPNRX		
	110	120	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

```

1  atgaaacctt tgatttttagg gcttgccgcc gtgttggttc tgtctgcctg
51  ccaagttcga aaagctcccg acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aatttttggtg gttccgccgc tgaacgagtc gcctgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga tttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggctggt cgattcccgc aacgggaaag agttgtggtc gggttcggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgccaa cagcctgacc gaccgcgggt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattcccg
601 aacggtatct tgaaaggtcc gagattcgtc gaagagcagc ccaaataa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAG AAAGCGCCCG ATTCGACTA CACGTCAATC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCCGCCCGC TTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGCGATCT TGAAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
	: : : : :					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	: : : : :					
g235	AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           |||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130      140      150      160      170      180

           190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           |||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
           190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATT TCGGCAATGA TCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACCTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

m235.pep  10      20      30      40      50      60
           MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
           |||||
a235      10      20      30      40      50      60
           MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

           70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFQKNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
           |||||
a235      70      80      90      100     110     120
           AAPLSEAGYYVFPAAVVEETFQKNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS

           130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           |||||
a235      130     140     150     160     170     180
           YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT

           190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           |||||
a235      190     200     210
           DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51  CGGTTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTACAGATAG CCGGCCATTT CTTCGCGCGC GGTAATTTTCG
251 GCTTCCGCCT GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAgTTC GGCTTCGGCT TTTTCGTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCCAACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGGCGGGC GCGGCTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGGAAAG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTGCAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCTT GTTGACCGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCCTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGCGCG ACGACGTGTC
951 CGATGGATTT CGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TGC CGCTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1  MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAAFAFFAV AGFGNGKFI
51  TDFHFCFRHQ QGKAQFFAQs IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLRAAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNNV FHGEVEGIAR IVTACQTLLO PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAO
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1  ..TTGCACGGAC GAACCGACGG TTTTGTGCGC GCGCAAAGGC TCGATGGCGG
51  CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCACT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCKTCTTCGC CGCCGCCGWT GayGTCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAACT GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACaTG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG AACTCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTT AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCG CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1  ..LHGRDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPSME
51  EDAVXFAXAX DVPRFFAGEA QNRNQNENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFAE RNxVfYgKVE XITRIVIAcQ TLLQLTCQYH
151 GVAVDFHHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236


```
m236.pep                                10      20      30  
                                  LHGRTDGFVGAQRLDGGGYRFAGFADCRPF  
                                   |:| | |:| | |:| | |:| | |:| |  
g236    FRHQQGKAQQFFAQSIQIAGHFFRRGNFGFRLLQGR TDS FVGAQRL DSGGCYCFARFADCRPF  
        60          70         80         90        100       110
```

40 50 60 70 80 90

```
m236.pep    FHQFGFGFFVDGRELVPSMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQGS LC  
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| :||| :| :| :|  
g236    FHQFGFGFFVDGRELVPSMEEDAVF AAADD VPRFF AGE A QN RC NQ EN QAARDVVQGGLR  
        120        130        140        150        160        170
```

100 110 120 130 140 150

```
m236.pep    AACMAVCFCGGVEAVFDDEVERTQVFRAERNXFVGKGVEXITRI VI ACQT LLQLTCQYH  
           ||   || ||||| ||||| ||:||| ||||| ||::| | :| | | ||||| ||:  
g236    AAAGA AV G FG G VE AV FD DE VER AQ VF RA ER NN VF H GE VEG I AR IVT AC QT LLQP PR O Y Q  
        180        190        200        210        220        230
```

160 170 180 190 200 210

```
m236.pep    GVAVDFHHIRLLHGIFNR IKVAQ VG KQAQGI ADTA VA EGYAF ED FF GN RQ FA AVIGRCR  
           ||||| ||||| ||||| ::| :| ||||| :| | | | | | | | | | | |  
g236    GVAVDFHHIRLLHGIFNR IKVA IQ GKQE AQ GI ADA AV AF G NA FED FF GN RQ FA AVIGGCR  
        240        250        260        270        280        290
```

220 230 240 250 259

```
m236.pep    PQAQDVCAEFVINL LRCNDVADGFRHFFAFAVDNETM GGQ LFIRRATH X  
           ||||| ||||| ::| :| ||||| ||||| :| :| :| :| | | | | :|  
g236    PQAQDVRAEVIDFLRDDVADGFR HFAAVLVNHE TVGQQL FIR CASHG  
        300        310        320        330        340
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```
a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCA
51  CGGTTTCATG GCCTGCAACC GCGCCACAT  CGCGGGTGTA GTGCCAGCAG
101 CGTTCGCATT TTTACCATTG ACTGGCTTTA CGCGCAACGG CAAGTTTCGT
151 GCCTACTTTT ACCTTCTGTT TAGACACCAG CAAAGCAAAG GCAATTCCTT
201 CGCCCAAAGC ATTACAGATAG CCGGCCATTT CTTCCGGCGC GGTAAATTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCCGGCG GCAAAGGCTC
301 GATGGCGGCG GTTACCGCTT CGCGGGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAGTTT GGCTTCGGCT TTTTCGTTGA TGGTCCGGAA CTCGTGCCAA
401 GTATGGAATA CACAGCTGTC TTCTCGCCG CGCCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCCGCTGCG
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGCGCGGGC GCGGCTGTCT
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTT TTTACGGCA AAGTGGAAGG
651 CATAACCGCG ATAAAAATCA CCGGCAACGC GTTCTTGCAG CCGCCTTGCC
701 AACACCAAGG ATATCGGCTC GATTTCACAC GTTACCGCCT GTTGCACGGC
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGTTA  CGCGCTTGAG GATTTCCTTG
851 GAAATCGCCA ATTCGCGGCT GTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCGGCG CCGAACTCGT TATACACTTC TTGCGCGCGC ACGACGTTGC
951 CGATGGATTG GCACATTTTG CGCCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTACGG CGCGCGACCC ATTGA
```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

a236.pep

1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAAFAFFTI	TGFSGNGKFA
51	AYFHFCFRHQ	QSKAQFFAQS	IQIAGHFFRR	GNFGFGLQGR	TDGFVGAQRL
101	DGGGYREAGF	ADCRPFFHQF	GFGFFVDGRE	LVPSMEKHAV	FCAAADDVPR
151	FFAGEAQNRK	NQENQAARDV	VQGGLRAAAG	AAVGFGGIEA	VFQDIEVERA
201	QVFRAERNHF	HGKGVGIGTR	IKITGNAFLQ	PPCQHQGIV	DFHHIRLLHG
251	IFNRIEVAQV	GKQKQAGIAD	TAVAFGYALE	DTFGNRQFAA	VIGGCRFPQAQ
301	DVRAELVIHF	LRRDDVADGF	RHFAPVLIHH	ETMGOOLFVR	RATH*

m236/a236 81.0% identity in 258 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq					
1	atgcggggaca	aggttgggcgg	taatatcgca	ctccccgcc	cacgaatat
51	cgattctaac	atcggcaagc	tgcggaaaaa	ctttaagcat	atcttggcgg
101	acaagctcgg	tcatcgcgc	aggattgtcg	ataaatctgt	tatccttacc
151	gccgaaaagc	agcctgcgt	ccgcgctgag	gcggtaatca	tccaaaaata
201	ggcggttgtc	gcatactgcc	ataattgttc	ggataagccc	ttttgtgcgc
251	gcgccaagg	gttcggtggc	aataataaag	gtgctgacgg	caatcgccct
301	gcgttccaaa	ggcgggaata	togggttcaa	accgacataa	gtattgacgg
351	catagaccac	atTTTTTtac	tgcgcgtgc	cttcgggcgt	gtaaaccagc
401	caaccgtttt	gatacgggtc	gatgcgcgtc	atcggggatt	gctcgaaaaa
451	ctgcgcgcg	gcttcggcag	cggcgctggc	aacaccaaac	gtgtaattga
501	gcggatgaag	atgcccgac	aagggatcga	actgtgcgcc	ttggtacata
551	tgcgtgtcaa	gctgctgttt	caactcggct	ttatcccaa	gttgataatg
601	actcgaccg	taatgcccgt	gggcgtgttc	atgccactgc	tgcaactctt
651	ccaatgctg	cggacggacg	gcaaccgtgg	cataaccgcg	ctgccaatcg
701	caatcgatgg	catgttttgcg	gacgcgttcg	tccaccagt	cgaccgcctg
751	caaagactgt	tgccaaaacc	attgcgcctg	ctccaagcgc	acctgttttt
801	caatttcccc	cataccgcag	gcgtagtcgc	tgataaacctg	cccgccactc
851	ctgccggacg	cgccgaagcc	gatacgtgcg	gcttccaaaa	cgacggcttc
901	atgtccgtgt	tccgccagcg	gcaatgcggt	acacaaaaccg	ctcaaaccgc
951	cgccgataat	gcaggttttcg	gcttttcagac	ggcattggag	tttcggataa
1001	acagtatcgc	gattaaccga	actaaaataa	taagaaggca	gatattcttg
1051	aaaatcaggg	cgaatcattg	tgtttgtctt	atcgggtata	tttcggacg
1101	gaatgatata	gactgtcggg	ccatatcgtc	caaacagaaa	atcggttga

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pep
1 MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51 AEKQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAQGGFGG NNGGADGNRL

```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
151 LRAFGSGAG NTQVIERMK MPQGIELCA LVHIAVKLLF QLGFI PKLIM
201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
301 MSVFRQRQCG TOTAQTAADN AGFGQTALE FRINSMRINR TKIIRQIFL
351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq

```

1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATACGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT
201 GGCGGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGCG
251 GCCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTCGGGCGT GTAAACCAGC
401 CAACCGTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT
451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCCAA GTGTAAGTGA
501 GCGGATGCAG GTGTCCGGAT AAGGGGTCGA ATTGTGCCCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
601 ACTCGCACCG TAATGCCGTT GGGCGTGTTT ATGCCACTGC TGCAACTCTT
651 CCCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
701 CAATCGACGG CATGTTTTCG GACGCGTTTC TCCACAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
801 CAATTTCCCC CATAACCGAG nCGTAATCGC TGATAACCTG CCCGCCACTC
851 CGTCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCAGGTGTA TTTTCGGACG
1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep

```

1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT
51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL
101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
151 LRTGFGSGTS DAQSVSERMQ VSGXGVLCF LVHIAVKLLF QLGFI PKLIM
201 TRTVMPLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRAET DTRGFQHNRF
301 MSLRQGCQS AQTTSAAAD TGIGFQTALK FRINSMRINR TEIIRQIFL
351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH TL RIVDKLVILTAEKQSAVRAE					
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH TR RIVDKFVILTAEKQPAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNNGGADSNRLAFQRPEYRVQTCISIDSIDH					
g237	AVIIQNMAVVAYCHIVADKPF CARAQFGGNNKGADGNRLAFQRPEYRVQTDISIDGIDH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVLCF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 885>:

```

a237.seq
1    ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51   CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAAGCA ATCTTGGCGG
101  ACAAGCTCGG TCATACGCGC GGGATTGTCTG ATAAACTCGT TATCCTTACC
151  GCCGAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAATAT
201  GACGGTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251  GCGCCCAAGG GTTCTGTGCG AATAATAAAG GTGCTGACAG CAATCGCCTT
301  GCGCTCCAA GGGTTGAATA TCGGATTCAA ACCGGCATAA GTATTGACGG
351  CGTACACCAG ATTTTTCGAT TCGAGCTGCTG CTTCGGGGGT GTAAACGAGC
401  CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAT
451  CTTGTAACCA GCTTCGGCAG CGGCGCGGGC GATGCCCAAC GTGTAATTGA
501  GCGGATGGAG ATGCCCGGAG AAGGGATCGA ACTGTGCGCC TTGGTACATA
551  TCGCTGTCAA GCTGCTGCTT CAGTTTCAGT TTATCCCAGA GTTGATAATG
601  AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCCATTGT TGCATTCTT
651  CCCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG TGCCAATCG
701  CAATCAATGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751  CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801  CAATTTCTCT CATACCGCAG GCGTAATCGC TGATAACCTG CCCGCCACTC
851  CGTCCCGACG CGCCGAAAAC GATACGCGCG GCTTCCAACA CACCGCTTTC
901  ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951  CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCGGAGC
1101 GAATGATACA GGCTGTCGAG CCATATCGTC CAACACAGAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 886; ORF 237.a>:

a237.p	1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
	51	AEKQSAVRAE	AVIIQNMVTV	AYCHIVADKP	FCTRAQGFGC	NNKGADSNRL
	101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAAFGG	VNQPTVLIRF	NAYHGRMLKN
	151	LRTSFGSGAG	DAQRVIERME	MPQGQIELCA	LVHIAVKLLL	QFSVIPELIM
	201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
	251	QRLLPKPLRL	LQTDLFNFEL	HTAGVIADNL	PATPSRRAET	DTRGFQHNRF
	301	MSLLRQGQCS	AQTTQSAADD	TGIGFQTALK	FRINSMRINR	TEIIRRQIFL
	351	KIRANHCVCF	IGYIFGRNDT	GCRAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	10	20	30	40	50	60
	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
m237.pep	70	80	90	100	110	120
	AVIIQNMAVVAYCHIVTDKPFPCARPQGFRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	70	80	90	100	110	120
	AVIIQNMTVVAYCHIVADKPFCTRAQGFSGNNKGADSNRLALQRLRYRIQTGISIDGVHQ					
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDARHRLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	130	140	150	160	170	180
	IFAFDAAFGGVNQPTVLIRFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFIPKLIIMTRTMPLGVFMPLQLFPMPLRTDGNRGITALPITIDGMFA					
a237	190	200	210	220	230	240
	LVHIAVKLLQFSVIPELIMSCTVIFLGVLMPLQLQFFPMPLRTDGNRGITALPIAINGMFA					
m237.pep	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLQLADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF					
a237	250	260	270	280	290	300
	DAFVHQFDRLQRLLPKPLRLQLADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF					
m237.pep	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVC					
a237	310	320	330	340	350	360
	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRROIFLKIRANHCVC					
m237.pep	370	380				
	IRCFGRNDTGCRAISSXQKIGX					
a237	370	380				
	IGYIFGRNDTGCRAISSKQKIGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctcgcggcag tgtaaataat cgggtttgcg ccgtccaaac
201 atttgatgca actgcggtcg gccccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggetatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccgtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 gggtatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gccccttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcggg ttttctcagc
601 cgtgcgggatg aagcaggaaa actgatatgg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caagggtcgg
701 ttaatccttt ttaacgggt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccggg cacagataga gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcaciaa cttgccgcgcg

```

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcaggtac ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaatTTTga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggttaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAIISMLH IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51 FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFLTg FQGVGIGAIT
251 DSAVSPVTDt AAQQTlQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHpN ITATAQTALA VAEAAgTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMqTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEga RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIOANFETYt IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTcATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CAcTACGAAC CGGGTGGTAA ATACCATCTG
151 TTGGTAATG CTCGCGGCAG TGTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTtATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAGCGGC GGTGTAGACG GCGGTTTtAC TGTTTACCAA CTTcATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ATTtATGTCAA
501 AGGAACtTCA ACAAAAAACAA AGACTAATAT TGTCCCTCAA GCCCATTtTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTtTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTcG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCcGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTtAGGAA AATTAAGTCC GGAAGCACAa CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCgG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTtTGAGAG GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAActGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTcACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTtAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

```

151 DYPPPPGGARD IYSYYVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
301 AKQWADAHPN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMQTL DGEMAGGNKP IKSLPNSAAE KRKQNFEEKFN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLQKGQAKD YLQQQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238 . pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAAISMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238 . pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCVAVQTFDATAVGPILPITHERTGFEVIGYETHFSGHGHEVHSPFDNHSDSKSTSDFSG					
	70	80	90	100	110	120
m238 . pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTKTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYPEPQGARDIYSYHIKGTSTKTINTVPQ					
	130	140	150	160	170	180
m238 . pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238 . pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
g238	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGINS					
	250	260	270	280	290	300
m238 . pep	310	320	330	340	350	360
	AKQWADAHPNITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL					
g238	ARQWADAHPNITATAQTALAVAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTV					
	310	320	330	340	350	360
m238 . pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAEKRKQNFEEKFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI - TSEGKANAATYPKLVNQLNEQNLNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
m238 . pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLDNSNGNAVKTGNLQKGQAKDY LQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTS GGWLSRDGTRQYRPPTEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTAAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACCTCTGA
351 TTTCAGCGGC GGCCTAGACG GTGGTTTTAC CGTTTACCAA CTTTCATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCCGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACTTCA AAAAAACAA AGAGTAATAT TGTTCCTCCG GCCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGCAG TAAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAAA TGGGATTGGG TAAAAAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGGKYHL
51 FGNARGSVKN RVYAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQOTLQGIN HLGNSPEAQ LAAATALQDS AFAVKDGIN
301 ARQWADAHN ITATAQTALA VAEAATTVWG GKKVELNPTK WDWKNTGYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ
```

m238/a238 91.9% identity in 385 aa overlap

m238.pep	10	20	30	40	50	60
	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVK
a238	10	20	30	40	50	60
	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVKN
m238.pep	70	80	90	100	110	120
	RVYAVQTFDA	TAVSPVLPIT	HERTGFEGV	IGYETHFSGH	GHEVHSPFDH	DSKSTSDFSG
a238	70	80	90	100	110	120
	RVYAVQTFDA	TAVGPILPIT	HERTGFEGI	IGYETHFSGH	GHEVHSPFDN	HSKSTSDFSG
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYYVKGT	STKTNTNIVPQ
a238	130	140	150	160	170	180
	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYYVKGT	STKTNSNIVPR
m238.pep	190	200	210	220	230	240
	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	190	200	210	220	230	240
	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
m238.pep	250	260	270	280	290	300
	FQGVGIGAIT	DSAVSPVTD	TAAQOTLQGI	NDLGKLSPEA	QLAAASLLQD	SAFAVKDGIN


```

a238      |||||
          FQGVGIGAITDSAVSPVTDTAQQOTLQGINHLGNLSPEAQLAAATALQDSFAFAVKDGIN
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHNPINITATAQTALSAEAAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a238      ARQWADAHNPINITATAQTALAVAEAAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNFENSNWSSASFDSVHKTLTPNAPGILSPDKVK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1   atgttccacc ataaaggtat tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgata gcttcgtgat tcgccaaacg cgcctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaagc ggaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcggaccg
301 gcagtccgct ccgccacacg caaaactgcg ctctcgccc tcgggttggc
351 ggcaatttcc gttcaccccg gctttaatgc cctgcccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgcc gccctcttcc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttaataaag
601 atgcggattg cctggaaggt gcgcgtcgca ggatcctgcc cccgctcgcg
651 agtacggacg tttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1   MFHHKGIARN RRMEVLFFCR RPDRFVIROT RLLQPHLR II LLQGDFLFFR
51  LVQSCEVEPV LVLHHLHNGKS GNAHRKQOKE IRFVHCRSDV FLCYYSIGIP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSRLLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWRL
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1   ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTTGTT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTG GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCCAGCG CGGCAGGGGC
451 GCGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGCACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCCGCTCGCG
651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTTGCGG GTTGATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CCGCGCGCAAT CCGGCGGCTa
751 AACCGCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239.pep
 1 MLHHKGXARN RXMEVLFFCR RPDRFVVRQT RLLOPHLRRI LLQGDFFLFFR
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
 101 AVRSATRKA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQRGRG
 151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
 201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
 251 NRSSP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRPDRFVVRQTRLLQPHLRRIILQGDFFLFFRLIQSCEIEPV					
g239	MFHHKGIARNRRMEVLFFCRPDRFVIRQTRLLQPHLRRIILQGDFFLFFRLVQSCEVEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCRSDVFLCYSGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIRRLNRSSPX					
g239	ATMARTIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

a239.seq

1	ATGCTCCACC	ATAAAGGTAT	TGCCCCGAAAC	CGGCGGATGG	AGGTTTGTGT
51	TTTCTGCCGC	CGCCCTGATC	GCTTCGTGGT	TCGCCAAACG	CGCCTGTTGC
101	AGCCTCATT	GCGCATAATC	CTGCTCCAAG	GCGATTTTCT	GTTTTTTCGC
151	CTTATCCAAA	GCTGTGAAGT	TGAGCCTGTA	CTGGTTTTGC	TGCATCACAA
201	CGGAAAAGC	GGAAACGCAC	ACCGCAAGCA	GCAGAAGGAA	ATTCAATTG
251	TTCATTGCCA	TTCAGACGTT	TTTCTCTGTG	ATTGTTCCGG	TATCGGACCG
301	GCACTCCGCT	CCGCCACACG	CAAAACCGCA	CTTCTCGCCC	TCGGATTGGC
351	GGCAATTTCC	GCCTCACCCG	GCTTTAATGC	CCTGCCCGCG	ATTTTCAGGG
401	GCGGCTCGGG	CAAATCCGCT	TCCCTGACCG	CCGCCAGCG	CGGCAGGGC
451	GCGTGTGCG	AATATTTTTT	GACAACTGC	TTCACAATGC	GGTCTTCCAA
501	CGAATGGAAA	GCAATGACCG	CCAAACGTCC	GCCCTCTTTC	AGACGACACA
551	TGACCTGCGG	CAATACTGCC	CCTACTTCTT	CAAGCTCGCG	GTTAATAAAG
601	ATGCGGATTG	CCTGGAAGGT	GCGCGTCGCA	GGATCCTGCC	CCCGCTCGCG
651	AGTACGGACG	TTTTGTGCCA	CGATCTGCGC	CAGCTTGCGG	GTTGTATCGA
701	TTGGACTTTC	CGCCCGTTGC	GCAACAATGG	CGCGCGCAAT	CTGGCGGCTA
751	AACCGCTCTT	CACCATAA			

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
 51 LIQSCEVEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKA LLALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

```

      10      20      30      40      50      60
m239.pep MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFFRLIQSCEIEPV
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRRIILQGDFFRLIQSCEVEPV
          10      20      30      40      50      60

      70      80      90     100     110     120
m239.pep LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS
          70      80      90     100     110     120

     130     140     150     160     170     180
m239.pep ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      ASPGFNALPAIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF
          130     140     150     160     170     180

     190     200     210     220     230     240
m239.pep RRHMTCGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a239      RRHMTCGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC
          190     200     210     220     230     240

      250
m239.pep ATMARAIIRRLNRSSPX
          ||||| ||||| ||||| |||||
a239      ATMARAIWRLNRSSPX
          250
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacattt cttcgggcgcc gaaacgcgca gacagtttgc
 51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacat gggatatcat gcgcacggga gacgggtccga ttttataagg
151 ctgcgtattc agccgttcgt tcaaatecgt ttgtcccga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac cagggttcgat catatcggtt
251 acggcacggt tgcgcccgtg ttcgctgtct gcccggccgg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcg gcttttgct gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcacaa caacttcgc gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagtcc aaaccttcct gacctttgcc
601 gtcaatatcg gtaaattcca tgacgtgtgc aaacagggtg cccatcgggg
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
 51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFLTFA
```

201 VNIGKSDDVC KQVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```
m240.seq
1   ATGATAGAAG TCATACATTT CTTCCGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGCGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GCGTTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

```
m240.pep
1   MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGT VAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFTFLTFVAV
201 NIGKSDDVCK QVAHRVMAF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

```
m240/g240

      10      20      30      40      50      59
m240.pep MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIG
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMGIIAHGRRSDFIRLRIQPFVQIG
      10      20      30      40      50      60

      60      70      80      90     100     110     119
m240.pep FARIQCLRNHKKRFD CRTGFDH IGYGT VAPLF AVCPAGPVGIVGGRIGQGEDFPRAGIQXH
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      FARIQCLRNHERFD CRTGFDH IGYGT VAPLF AVCPAGSVGIVGGRIGQGEDFPRAGIQNH
      70      80      90     100     110     120

      120     130     140     150     160     170     179
m240.pep HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      HRS GFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRCFIARGVQAVHNIALPVPQNNFR
      130     140     150     160     170     180

      180     190     200     210     220
m240.pep AVFAMQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAFX
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      AVFAIQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAF
      190     200     210     220
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

```
a240.seq
1   ATGATAGAAG TCATACATTT CTTCCGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
```

551

```

251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQND FRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQND FRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFIARGVQAVHNIALPVPQND FRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 ArACCACCAC CGTTCCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATGTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI OKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTCCTC ATCGGATGCA TCGCGCACGC TTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA TTGTTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFDNR EHARIFDTDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV OKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVVMTVRAVDMTVCDL	IGCIAHAFNC	
g241						
	70	80	90	100	110	120
m241.pep	40	50	60	70	80	90
	SLKADFHACQRMVAVVHRLAVGNIGYTID	NIAGFRIVGFKHHA	DFDNRERHARIFD	TDQ		
g241						
	130	140	150	160	170	180
m241.pep	100	110	120	130	140	150
	LRILLAERIVGRQRHIDRIAGILTVQRLFH	QRENAVVTAVQIRNRFFGFV	OKLIVGIIHL			
g241						
	190	200	210	220	230	240
m241.pep	160	170				
	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241						
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACGCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAATCA
151 GCGAACCAGC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCCTT TTCAGACGGC

```

251	ATCAGATACC	TCCAAGCTGC	CGGCAATCAG	TGGTGGTGAT	GACCGTGCGG
301	ACCGTGGACA	TGACCGTGTG	CGATTTCTC	ATCGGATGCA	TCGCGCACAC
351	TTTCAACCGT	AGCCTTAAAG	CGGATTTTCA	TGCCTGCCAA	AGGATGGTTG
401	CCGTCCACCA	CGCTTCTACC	GTCCGGCAACA	TCGGTTACAC	GATAGACGAC
451	AACATCGCCG	GTTTTCAGGAT	CGTCGGCTTC	AAACATCATG	CCTGACTTCGA
501	CTTCAACAGG	GAACACGCCC	GCATCTTCAA	TACGGACAA	CTCCGGATCC
551	TGCTCGCCGA	ACGCATCGTC	GGGCGAAAGC	GCCACATCGA	CCGTATCGCC
601	GGCATCCTTA	CCGTGCAACG	CCTCTTCCAC	CAAAGGAAA	ATGCCGTCTG
651	AACCGCCGTG	CAGATACGCA	ATCGGTTCTT	CGGTTTGTG	CAAAGCTGA
701	TGTGTTGGCAT	CATACATCTC	ATAATGCAGC	GAAACCACGG	AATTCTTCAC
751	GATAGCCATA	TTTGTCTTTT	CAGGAACAGC	AGATTAATTA	CAGGCGCATT
801	CTAA				

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

a241.pep

1	MPTRPTRA	AK	HPTPPTWL	QT	AYCPRPPY	RP	PSVQTHTP	HE	PASSTCAAKS
51	ANRRENFH	NA	QPTYLLHPS	N	KMPSEMEQ	TL	FRRHQI	PPSC	RQSVVMTVR
101	TVDMTVC	DFL	IGCIAHTF	NR	SLKADFH	ACQ	RMVAVVH	RLT	VGNIGYTIDD
151	NIAGFRI	VG	KHHADF	FN	EHARIF	NTDQ	LRILLA	ERIV	GRKRHIDRIA
201	GILTVQRL	LFH	QREN	AV	VTAV		QIRNR	FFGFV	<u>QKLIVGIIHL</u>
251	DSHICP	FRNS	RLTGAF	*					IMQRNHGILH

m241/a241 96.0% identity in 177 aa overlap

m241.pep				10	20	30
				RQSVVVM	TVRAVDM	TVCDFLIGCIAHAFNC
a241						
				QPTYLLHPSN	KMPSEMEQ	TLFRRHQI
	70	80	90	100	110	120
m241.pep	40	50	60	70	80	90
	SLKADFHACQ	RMVAVHH	RLAVGNIG	YTI	DDNIAGF	RIVGFKHH
a241	SLKADFHACQ	RMVAVHH	RLTVGNIG	YTI	DDNIAGF	RIVGFKHH
	130	140	150	160	170	180
m241.pep	100	110	120	130	140	150
	LRILLAERIV	GRQRHID	RIAGILT	VQRLFH	QREN	AVVTAVQ
a241	LRILLAERIV	GRKRHID	RIAGILT	VQRLFH	QREN	AVVTAVQ
	190	200	210	220	230	240
m241.pep	160	170				
	IMQRNHGIF	HDSHICP	FRNSRL	LITGA	FX	
a241	IMQRNHGIL	HDSHICP	FRNSRL	LITGA	FX	
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

g241-1.seq

1	ATGATAGAA	TCATACATT	CTTCGGCACC	GAAACGCGCA	GACAGTTTGC
51	TTGTGCCGAC	GTTGGACGAT	TTCTGCATGA	TGCCGCGCAC	ATCCAAAGAG
101	GGGTAAACAT	GGGTATCGCG	CACGGGAGGAC	GGTCCGATT	TATAAGGCTG
151	CGTATTACG	CGTTTCGTTCA	AATCGGTTAT	GCCCGCATCC	AATGCTCTCG
201	CAATCACAA	CGGTTTGATT	GCCGAACCGG	GTTTCGATCAT	ATCGGTTACG
251	GCACGGTTTG	GCCCGTGTTG	CTGTGTCGCC	CGCCCGGGCG	TGTTGGGATC
301	TGAGCGGGCG	GATTATGGCCA	AGGCCAGGAT	TTCCCCCGTG	CGGGCATCCA
351	ArACCACCAC	CGTTCGGGCT	TTTGCTTGAT	GGTATTCGAC	CGCCTTGTTT
401	AACCTCTCAT	AGGCCAAGGT	CTGAATCCTC	TGATCGAGTG	AAAGGATGAT
451	GTCTTTGCCG	TTTTTCGGGG	CTTTAKTGCC	CGGGGAGTCC	AGCTGTGCCA
501	CAATATTGCC	TCGCCGGTCC	CGCAAACGCA	CTTCCGCGCC	GTTCTCGCCA
551	TGCAAGCTGT	CTTCAAGCGA	AAGTTCCAAA	CCTTCTGAC	CTTTGCCGTC
601	AATATCGGTA	AATCCGATGA	CGTGTCAAA	CAGGTTGCCC	ATCGGGTAAT
651	GGCGTTTTAA				

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

g241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMTVR
101 TVDMTVCDLF IGCIHAFAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCTT CAACCTGCGC GGCAAAATCA
151 GCGAACCCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCTTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGC GG
301 GCCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCCCGGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pap

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMTVR
101 AVDMTVCDLF IGCIHAFAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHADEFDFNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pap	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pap	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMTVRAVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pap	SLKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVGFKHHADDFNREHARIFDQDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDDNIAGFRIVRFKHTDLDFNRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pap	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pap	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```



```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAACCCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCAGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRAAK HPTPTWLQT AYCPRPPYRP PSVQTHPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	: : : : :					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSQSVVMTVRVAVDMTVCDFLIGCIAHAFNC					
a241	: : : : :					
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSNKMPSETEQLFRRHQIPPSQSVVMTVRVAVDMTVCDFLIGCIAHAFNC					
a241	: : : : :					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVHRLAVGNIGYTIDNIAAGFRIVGFKHHADFDENREHARIFDNTDQ					
a241	: : : : :					
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQRMVAVHRLAVGNIGYTIDNIAAGFRIVGFKHHADFDENREHARIFDNTDQ					
a241	: : : : :					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
a241	: : : : :					
	190	200	210	220	230	240
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
a241	: : : : :					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	: : :					
	250	260				
m241-1.pep	IMQRNHGILHDSHICPFRNSRLITGAFX					
a241	: : :					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgtc gatttcgctg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccc cggtattcgc
201 tttcgtcgcg cacgcgcccc aaggccatac ggacataatt ccgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgccacgcg ccggaggggc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttgagcgg
351 cgaggtatte caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcgggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgct gatgtagttg cgtacgacgg

```

```

501 tggattcggc agacatcggc ggcattcattt tgagttttttt cagttcggac
551 aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgtc ttcttcgccc aattccttgc
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701 atttggcgtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcgttgcc ccagtttcaa ctgcaaatgc
851 gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pep

```

1 MIGELVVLFFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVV YACFCHILQN
51 LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFDGFDA QRGFAHARRA
101 DQTONRTFEL VHTFLDGEVF QNPFFDFFQA VVVGIIHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHFEFF QFGQAFFFRF FGHTRLFDAC
201 LOGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQQE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

```

1 ATGATCGGCA AACTTGTGTG TTTGTTTCGG ATCGAGCACT TCGAGCAACG
51 CGCTGGCGGG ATCGCCTCGG AAGTCGTTAC CCAATTTGTC GATTTTCGTCG
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTTCGC
201 TTTCGTCGCG CACGCCGCCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTCGCC CAAAGAGGTT TTGCCCACGC CCGGAGGGCC
301 GACCAGGCAC AGAATCGGCG CTTTGAGTTT GTCCATACGT TTTTGAGCGG
351 CGAGGTATTC CAAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATTT
451 TTCTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCGCTTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGCA TCCAGTTCGC CGTTTTTCGTC TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTTC TTCAGATAAT ATTCGCGCTG GGATTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATTT
801 CGGGAATTTT CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242.pep

```

1 MIGKLVVLFG IEHFEQRAGG IASEVVTQFV DFVEQEQQVF HAGFCHILQN
51 LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGFDA QRGFAHARRA
101 DQAQNRAFEF VHTFLDGEVF QNPFFDFFQA VVVGIIHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFELF QFGQAFFFRF FGHTRLFDIC
201 FQGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQQE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

```

          10      20      30      40      50      60
m242.pep  MIGKLVVLFGIEHFEQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA
          |||:||||| ||||:||||| :||:||||| |||: |||||:|||||:
g242      MIGELVVLFFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVSYACFCHILQNLGHRADIGT
          10      20      30      40      50      60

          70      80      90      100     110     120
m242.pep  AVSPDFAFVAHAAQSHADIFPPRCFGDGFQAQRGFAHARRADQAQNRAFEFVHTFLDGEVF
          || |||||:|||||:|:|||||:|||||:|||||:|||||:|||||:
g242      AVPADFAFVAHAAQGHDTIFPPRCFGDGFQAQRGFAHARRADQTONRTFELVHTFLDGEVF
          70      80      90      100     110     120

```

m242 . pep

g242

m242.pep

q242

m242.ppe

q242

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID:921>:

a242.seq

1	ATGATCGGCG	AACTTGTGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAACG
51	CGCTGGCGGG	ATCGCCCCGG	AAGTCGCTAN	CCAATTGTGC	GATTTCGTCG
101	AGCAGGAACA	ATGGGTTTTT	TACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
151	CTTACCGGGC	ATGGAGCCGA	TATAGGTGCG	CGGGTGTCCC	CGGATTTTCG
201	TTTCGTGCGC	CACGCGCCCC	AAAGCCATGC	GGACATATTT	CCGCCCGGTT
251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCCACGC	CTGGAGGGCC
301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTTTGACCG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCC	GTAGTGGTCT
401	GTATCCAGCA	CCAATCGCGC	TTTGCGGATG	TCTTTGCTGA	CGCGGGATTG
451	TTTCTTCCAC	GGCAGTTCGA	GCAGGGTGTC	GATGTAGATT	CGTAGCAGCG
501	TGGATTCGCG	AGACATCGGC	GGCATCATTT	TGAGCTTTTT	CAGTTCGGAC
551	AGGCATTTTT	CTTCGCTTTC	TTTGGTCATA	CCCGCCTTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGGCC	AGTTCTTTGT
651	GTATCGCTTT	AATCTGTTTC	TTCCAGATAAT	ATTCCGCGTG	GGATTTTTTC
701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
801	CGGGAATTTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
851	GCTGCAGCCG	TATCGTTTAG			

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242.pwp

1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
101	DQAGNRAFEF	VHTFLDGEVF	QNPFFDFFQA	VVVGIQHQSG	FGDVADAGF
151	FLPRQFEQGV	DVVAYDDGGF	RHRRHHEFLF	QFGQAFFFRF	FGHTRLFDIC
201	<u>FQGIQFAVFV</u>	<u>FFAQDFVYRF</u>	<u>NLFVQIIFAL</u>	<u>GGFHAFDAS</u>	<u>AYAFFGLHNV</u>
251	EFGFOLCQOE	FHPADFVGNF	ONLLALROFO	LOMRCDRIG*	

m242/a242 95.2% identity in 289 aa overlap

m242.pep

a242

m242.per

a242

m242.pep

558

```

a242      QNPFDFDFQAVVVGIIQHSGFGDVFADAGFFLPRQFEQGVVDVAYDGGFGRRHRRHFFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLEDFICFQGIQFAVFVFFAQFFVYRFNLFVQIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFGHTRLEDFICFQGIQFAVFVFFAQFFVYRFNLFVQIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFPFADFNGFNQNLALRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHFPFADFNGFNQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcc cgAGTTaccg CCGATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTT
301 TCATCAACGA CGGCGCGCGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51 IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGCGCGCGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

m243/g243

```

           10      20      30      40      50      60
m243.pep  MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||
g243      MVIVWLPELPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1 ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1 MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSEFLF
101 SSTTGAUTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELP	PMPATMGIS	AXSATIFS	MLPSNAP	ITRLARKA	VQRLTASHIQXFFTESHT
a243	MVIVWLPELP	PMPATMGIS	AAASATIFS	MLPSNAP	ITRLARKA	VQRLTASHIQRFLTESKT
	70	80	90	100	110	
m243.pep	GANRSSSSCK	PAIFNISAS	DSSRITST	ISSMVILP	MSFLFSST	TGAVTKSX
a243	GANKSSSSCK	PAIFNISAS	DSSRITST	ISSVTLP	MSFLFSST	TGAVTKSX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1 atgccgcctg aagcccggcc ggccgggttc gacggcattg ccgctttact
51 tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcatcgccct atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttccac ggcaaaactt tgcggcgga acttgtgctg
451 atcggcaatt tcctgctggt ggccggcgcc caggttttgc tcgtttgcca
501 aagcgcgag ttgttcgtct tcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgctcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1 MPPEARPAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LPCHRNHSRA
51 QHTVGQGITL LHHTNHGIGF LLTGHLRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFLRFQL GNPLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSGYPSKIR
251 TFSRNFQORQ EISHPPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

```

1  ATGCCGTCTG AAGCCCGACA GGC GG GTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCT CTTTCATCACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GGCGGCGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTCTT GCACACCGTC
601 CGCATTTTCT ACTGTTTTCGA CGGTTTCCAC CGCCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAakCAGAGA ATTTCAAAT CATTTTCAAA
801 TCCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

m244.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLLCFLFAHI VSLKTNWWSK SSYYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

m244.pep	10	20	30	40	50	60
	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLPCHRNHSRAQHTVGQGITL					
	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244.pep	130	140	150	160	170	180
	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVFQLRFQL					
	130	140	150	160	170	180
m244.pep	190	200	210	220	230	240
	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTLLLLCLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFTLLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	250	260	270			
	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXYRRX					
g244	KSGYYPSKIRTFSRNFKQREISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGCTCTG AAGCCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC  TTCAGGCTTC  CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG  TCGGACAGCG  TATAACCCTT CTCATCACG  CCCACCACGG
201 TATTGGGTTT  CTGTTTCGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT  TATCGCCCGC  TTTAGGATTG ATTCCTTGA  TTTGCGTAGC
301 ATCAAATGCT  TTCTGCAACT  CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA  ATTGCCGCTC  TGATCCAAA  GCGCCATTTC CAGATAATCC
401 TTGACCGGCA  GCATTTCCAC  GGCAAACCTT TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT  TCCTGCTGGT  GCGGGCGGCG CAGGTTTTTG  TCGTTTGCCA
501 AAGCGCGCAG  CTGCTCGTCT  TTCAACTGCG CTTCCAGCTC  GGCAATCCGC
551 GCCTGCAAAT  CCTCATAAGC  CGGCTCTGCG GCAGCCTGTT  CCTGCACACC
601 GTCCGCATTT  CCTACTGTCT  CGACGGTTTC CACCGCCTCC  ACATTTTCAA
651 CCGCTTCTTC  ACTGTTTTGC  TGCTGTGTCT GTTCGCTCAT  ATCGTATCCC
701 TTAAACAAA  TTGGAATCA  AAATCCAGTT ATTACCCGCG  CAAGATAAGG
751 ACATTTTCAA  GAAACTTCAA  GCAAAGGCAG AGAATTTCAA  ATTCATTTTC
801 AAATCCCCTA  CCGAAAAAAT  AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTONALQEI NQIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRQLILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

m244.pep	10	20	30	40	50	60
a244	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
a244	70	80	90	100	110	120
m244.pep	130	140	150	160	170	179
a244	130	140	150	160	170	180
m244.pep	180	190	200	210	220	230
a244	180	190	200	210	220	230
m244.pep	240	250	260	270		
a244	240	250	260	270		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgcctg aagccccggc gccggggttca gacggcattg cgcgtttact
```

```

51  tcgacggtt  tatacgcaaa  acgcgcttca  ggaaataaat  cagattattc
101  cccagacgcc  ttcaggcttc  cttccgtgcc  accgtaacca  tagccgggcg
151  caacacacgg  tcggacaggg  tataaccctt  cttcatcaca  ccaaccacgg
201  tattgggttc  ctgctcactg  gccaccgcct  gcacgcctg  atggatattc
251  ggatcgagct  tatcgccgc  tttaggattg  atttccttga  tttgctggc
301  atcaaacgcc  ttctgcaact  cattcaaagt  catctgcaca  cccattttca
351  gcgcatcgaa  attaccgctc  tgatccaaaa  gcgccatttc  cagataatcc
401  ttgaccggca  acattttccac  ggcaaaacttc  tgtccggcga  acttgtgcgt
451  atcggcaatt  tcctgctggt  ggcgcgggcg  caggttttgc  tcgtttgcca
501  aagcgcgcag  ttgttcgtct  ttcaactgcg  cttccagctc  ggcaatccgc
551  gcctgcaaat  cctcataagc  cggctcggcg  gcagcctggt  cctgtacacc
601  gtccgcattt  cctactgtct  cgacgggttc  caccgcctcc  acattttcaa
651  ccgcttcttc  actgttttgc  tgctgtgtct  gttcgtcat  atcgtatccc
701  tcaaaacaaa  ttggaaatca  aaatccggtt  attaccgag  caagataagg
751  acattttcaa  gaaacttcaa  gcaaaggcag  gaaatttcac  atccgcgcgc
801  gaatacccta  ccgcaaaaac  catataaacg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LPCHRNHSRA
51  QHTVGQGITL  LHHTNHGIGF  LLTGHRHLRL  MDIRIELIAR  FRIDFLDLRG
101  IKRLQLIQS  HLHTHFQRIE  ITALIQKRHF  QIILDRQHFH  GKLLSGELVR
151  IGNFLLVAAA  QVLLVCQSAQ  LFVFQLRFLQ  GNPRLQILIS  RLGGSFLYLT
201  VRISYCLDGF  HRLHIFNRFF  TVLLCLFAH  IVSLKTNWKS  KSGYYPKIR
251  TFSRNFQQRQ  EISHPPPNTL  PQKPYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGCTCG  AAGCCCGACA  GCGCGGTTCA  GACGGCATTG  CCGCTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA  GGAAATAAAT  CAGATTATTC
101  CCCAGACGCC  TTCAGGCTTC  CTTCTGCGCC  ACCGTAACCA  TAGCCGGGCG
151  CAACACGCGG  TCGGACAGCG  TATAACCCTT  CTTTCATCACA  CCCACCACGG
201  TATTCGCTCG  CTGTTCTGCT  GCCACCGCCT  GCATCGCCTG  ATGGATATTC
251  GGATCGAGCT  TATCGCCCGC  TTTAGGGTTG  ATTTCCCTGA  TTTGCGTAGC
301  ATCAATGCT  TCTGCAACT  CGTTCAAAGT  CATCTGCACG  CCCATTTTCA
351  GCGCATCGAA  ATTGCCGCTC  TGATCCAAA  GCGCCATTTC  CAGATAATCC
401  TTGACCGGCA  GCATTTCCAC  GGCAAACTTC  TGTCCGGCGA  ACTTGTGCGT
451  ATCCGCAATT  TyCTGCTGGT  GCGGCGGCG  CAGGTTTTGC  TCGTTTGCCA
501  AAGCGCGCTG  CTCGTCTTTC  AACTGCGTT  CCAGCTCGGC  AATCCGCGCC
551  TGCAATCCT  CATAAGCCGG  CTCTGCGGCA  GCCTGTTCTT  GCACACCGTC
601  CGCATTTCT  ACTGTTTCGA  CGGTTTCCAC  CGCCTCCACA  TTTTCAACCG
651  CTTCTTCACT  GTTTTGCTGC  TGTGTCTGTT  CGCTCATATC  GTATCCCTTA
701  AAACAAATTG  GAAATCAAAA  TCCAGTTATT  ACCCGCGCAA  GATAAGGACA
751  TTTTCAAGAA  ACTTCAAKCA  AAKCAGAGA  ATTTCAAATT  CATTITCAAA
801  TCCCCTACCG  AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101  IKCFLLQVQS  HLHAHFQRIE  IAALIQKRHF  QIILDRQHFH  GKLLSGELVR
151  IRNFLLVAAA  QVLLVCQSAL  LVFQLRFQLG  NPRLQILISR  LCGSLFLHTV
201  RISYCFDGFH  RLHIFNRFFT  VLLCLFAHI  VSLKTNWKS  SSIYPRKIRT
251  FSRNFXQXQR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHRNHSRAQHTVGQGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLQVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHHTHFQRIE					
	70	80	90	100	110	120

a244-1.seq

1	ATGCCGCTCTG	AAGCCCGACA	GGCGGGTTCA	GACGGCATTG	CCGCTTTACT
51	TCGATCGGTT	TATACGCAAA	ACGCGCTTCA	GGAAATAAAT	CAGATTATTC
101	CCGAGACGCC	TTCAGGCTTC	CTTCTGTGCC	ACCGTAACCA	TAGCCGGGCG
151	CAACACGCGG	TCGGACACGC	TATAACCTTT	CTTCATCAGC	GCACCACCGG
201	TATTGGGTTC	CTGTTTCGTT	GCCACGCGTT	GCATCGCCTG	ATGGATATTC
251	GGATCGAGTT	TATCGCCCGC	TTTAGGATTC	ATTTCTCTGA	TTTGCGTAGC
301	ATCAAAATGCT	TTCTGCAACT	CGTTCAAAGT	CATCTGCAGC	CCCATTTTCA
351	GCGCATCGAA	ATTGCCGCTC	TGATCCAAAA	GCGCCATTTT	CAGATAATCC
401	TTGACCGGCA	GCATTCTCCAC	GGCAAACCTT	TGTCGGGGCA	ACTGTGGGTA
451	ATCCGCAATC	TCTCTGCTGGT	GCGCGCGGCG	CAGGTTTTCG	TCTGTTGGCA
501	AAGCGCGCAG	CTGCTCGTCT	TTCAACTGCG	CTTCCAGCTC	GGCAATCCGC
551	GCCTGCAAAAT	CCTCAATAAGC	CGGCTCTGGC	CAGCCGCTGT	CCTGCACACC
601	CTCCGCACTT	CTTACTGTCT	CGACGGTTTC	GACCGCTCC	ACATTTTCAA
651	CGCCTTCTTC	ACTGTTTTGC	TGCTGTGTCT	GTTGCTCAT	ATCGTATCCC
701	TTAAACCAAA	TGGGAAATCA	AAATCCAGTT	ATTACCCGCG	CAAGATAAGG
751	ACATTTTCAA	GAACCTTCAA	GCAAAGGCAG	AGAATTTCAA	ATTCATTTTC
801	AAATCCCTTA	CCGAAAAAAT	AA		

a244-1.pgp

1	MPSEARQAGS	DGIAALLRSV	YTQNALQEIN	QIIPQTPSGF	LLCHRNHSRA
51	QHAVQGQRITL	LLHAHHGGIGF	LFACHLRHRL	MDRIELIETAR	FRIDFLDELRS
101	IKCFLQLQVS	HLHAAHPQIE	IAALQKRHF	QIILDRQHEH	KGILLSGLVLR
151	IRNFLVAA	<u>QVLLVCQSAQ</u>	<u>LLVFQLRFQL</u>	GNPRQLILIS	RLCGSLFLHT
201	VRISYCLDGF	HLRHTFNRF	<u>TVLLCLLFAH</u>	IVSLKTNWKS	KSSYYPRKIR
251	TFSRNFKQGR	RISNFSNPL	PKK**		

m244-1/a244-1 96.8% identity in 274 aa overlap

		10	20	30	40	50	60
m244-1.pep		MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1		MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
		10	20	30	40	50	60
		70	80	90	100	110	120
m244-1.pep		LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFQLVQSHLHAHFQRIE					
		: :					
a244-1		LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFQLVQSHLHAHFQRIE					
		70	80	90	100	110	120
		130	140	150	160	170	179
m244-1.pep		IAALIQRHFQIILDRQHFGKLLSGELVIRIENFLLVAAQVLLVCQSA-LLVFQLRFQL					
a244-1		IAALIQRHFQIILDRQHFGKLLSGELVIRIENFLLVAAQVLLVCQSAQLLVFQLRFQL					
		130	140	150	160	170	180
		180	190	200	210	220	239
m244-1.pep		GNPRLQILISRLCGSLFLHTVRIISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244-1		GNPRLQILISRLCGSLFLHTVRIISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
		190	200	210	220	230	240

240 250 260 270
 m244-1.pep KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXX
 |||||
 a244-1 KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKXX
 250 260 270

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 941>:

```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgccct tcggttttcga
51  ccagacacag cgtgcccggt tcggcaacgg cgaagtttac gccgctcaag
101 cgcacatcgg cagtgcgtgta aatatcgcgc agggcttttgc gggcgaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgc tgtgcccaggg ttttggtgga
201 acagttcgct gacctgttct ttggttttat ggattgcggg catcacgata
251 tgggtcggtt tttcgccctgc catttggaag ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataattggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggtt
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtactttc acgcccact tagtcagggt ttcttccaac tgctccagca
501 gcgcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 942; ORF 246.ng>:

g246.pep

1	MYGRNGSTQA	AVAFVFDQTQ	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFPAD	HGFAPDHQLA	VFGCDDVVDN	LAGFGRGFRP
151	VYFHAQLSQV	FFQLLQQRG*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 943>:

```
m246.seq (partial)
1 ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51 CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACTCAAAC
101 CGACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTCAGCGGC GTACCGAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACGATAT
251 GGGTCGGTTT TTCGCTGCC ATTGGACGA TGAACTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGCTTT TGCTTCAAGA TAATGrTTCA GCTCGATTTC
351 CTCGCTGACC ATCGATTTCG CTTTGACCAT CAGCTTGC GG TTTTGGCTG
401 TGATGATGTC GTGGATAATT TGGCAGGCTT CGGTCGGGGT TTCTGCCCG...
```

This corresponds to the amino acid sequence <SEQ ID 944; ORF 246>:

```
m246.pep (partial)
      1 MHGRYGGTQA TVAFVFHQQT RTCFSNGKVY ATQTDIGSAV NIAQCFTGEA
     51 GQLVYIVCQR RTEVLVEQFA NLFFGFVDSR HHDMMGRFFAC HLDDELAQVA
    101 FYRFNAFCFK IMXQLDFLAD HRFAFDHQLA VFGCDDVVDN LAGFGRGFCE...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

m246/g246

	10	20	30	40	50	60
m246.pep	MHG	RYGG	TQAT	VA	VF	HF
	10	20	30	40	50	60
g246	MYGR	NGST	QAAV	AF	VF	DF
	10	20	30	40	50	60
m246.pep	RTE	VL	VE	QF	AN	LF
	10	20	30	40	50	60
g246	CAE	VL	VE	QF	AD	LF

565

	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1 ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTCCA
51 CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAA
101 CCGACATCGG CAGTGCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCAAGTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTAT GGATTGCGGG CATCACGATA
251 TGGGTCGGTT TTTCACCTGC CATTGGACG ATGAACGCG CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTG CCTTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGGCCGGTG TTTCCGCCCA
451 GTGTACTTTT ACGCCCAACT TGGTCAGGTT TTCTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1 MHGRNGGTQA TVAFVFHQTO RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51 GQLVYVVR*R CAEVLVEQFA NLFFGFMDCG HHDMGRFFTC HLDDELAQVA
101 FHRENAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVVDD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQTRTCFSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQTRTCFSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCHLDELAQVAFHRENAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1 atgaaacgta aaatgctaaa cgtaccaaag ggcggttatg atggtatgaa
51 gggttttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccggaa attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaatgtgc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaaactcaa
301 tctaaccctg caaaacccgg tgccaaacaa gaaaatcccc ttttttctt
351 aaaaaggagc ggcattggata aacaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggtatcg atgatcttga tgcgagtgtg gagactgttg tagtcagcag
501 ctgttccaaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatc

```

g247.pcp

m247.seq (partial)

m247.pep (partial)

m247/g247

BNSDOCID: <WO 8857280A2 | >

```

a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCCTGATGGC  GGTCCGATCG  AGTTACTTCA  CATCCCGGAA  ATTAAATGAT
151 GCGGCAACAG  AGCGTCTTTC  GCGCGAACAG  GATTTCGGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAAC
301 CAACATGTCC  CTGTAAAACC  CGGTGCCAAA  CAAGAAAATC  CCCTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAAATTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAT  ATCCGGGTTT  TGCCAGGGCT
451 CGTCCGGCAT  TGATTTTCCA  ATACGGCATC  GATGATCTTG  ATGCCAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAAGAGTG  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTCGGC  AGGATTGCCG  GTAGGAAGG  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGGT  AATCCTCAGT  TGCTCGTGAA  AAGAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CTATGTTTCC  GACTGTCCTG  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATT  GACAGCTCCA
851 CAAATGCTGT  TACGCCCGCC  GGGGTGGAGT  TTTATTTCAG  TANCGGTACT
901 GATACCAAGA  TTGCCGCTTC  TTCAGACAA  CATATTATTG  CTTACCGTAT
951 CGATGCGACA  ATACGGCGGG  GAAATGTATG  CGCAAACAGA  ACACTTTGA

```

a247.pep	1	MRRKMLNVPK	GNYDGMKGFT	IEFLVAGML	SMIVLMAVGS	SYFTSRKLND
	51	AA NER LSAQQ	DLR NA ATLIV	RDARMAGGFG	CFNM SI EHTKN	DIIVDPSKQT
	101	QHPVVKPGAK	QENPLFSLEW	ANTNNTNNNT	AKLIPIAESTK	DIKYPGFAQAT
	151	RPALIFQYGI	DDL D ASAETV	VVSSCSKIAK	PGKKISTLQE	AKSALQITND
	201	DKQNGNITRQ	RHVVNAYAVG	RIAGEEGLFR	FQLDDKGKKG	NPQLLVKKIR
	251	HKVRYIIVS	DCPEDDDAGK	EEKFKYTGTF	DSSTNAVTPA	GVEVLLSXGT
	301	DTKIAASSDN	HIYAYRIDAT	IRGGNVCANR	TL*	

```

      10          20          30          40          50          60
m247.pep  XRRKMLNVXXGSYDGMKGFTTIEFLVAGLLSMIVLMAVGSSYFTRSRKLNDAAANERLAAQQ
           ||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a247      MRRKMLNVPKGNIDGMKGFTTIEFLVAGMLSMIVLMAVGSSYFTRSRKLNDAAANERLSAQQ
           10          20          30          40          50          60

      70          80          90          100
m247.pep  DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNPFSLK-
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a247      DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDP SKQTQHVPVKPGAKQENPLFSLEW
           70          80          90          100          110          120

      110         120         130         140         150         160
m247.pep  -----RNGIDKLIPIAESNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK
           |: |||||::||:| :| :| |||||::||:| :| |||||:|:|
a247      ANTNTNTNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDAEETVVVSSCSKI AK
           130         140         150         160         170         180

```

	170	180	190	200	210	220
m247.pep	PGKQIPTLED	AKKELKIPDQ	KEQNGNIARQ	RHVVNAYAVG	RIADEESLFR	FQLDDKGKW
a247	PGKKISTLQEA	KSALQITNDDK	-QNGNITRQRH	VVNAYAVGRI	AGEEGLFRFQ	LDDKGKW
	190	200	210	220	230	
m247.pep	GNPQL					
a247	GNPQLLVKKIR	HMKVRYIYVSD	CPEDDDAGKEE	KFKYTGTFDS	SSTNAVTPAG	VEVLLSXG
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1   CCCGGTGCCA AACAAGAAAA TCCCCTTTTT TCCTTAAAAA GGAGCGGCAT
51  GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGAT ATGGATGTGC GGTATATTTA TGTTCCTGGT
451 TGTCTGAAG ATGAAGATGC CGGCAAAGAG GAAAAATTCA GATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTAC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TCGACAATA CGCGGGGGAA ATGTATGCGC
651 AAACAGAACA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1   P GAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYQIDD
51  L DASAETVVV SSSSKIAPKG KKISTLQEA SALQITNDDK QNGNITRQKH
101 V VNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 C PPEDEAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIAASSDNS
201 I YAYRINATI RGNVNCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1   ATGAGACGTA AATAGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAACAG AGCGTCTTGC CGCGCAACAG GATTTCGCGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCCTAATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTT CTTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTC ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTGCACAGCG CCCAAAATGC
801 TGTTACGCCG GCCGGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACCGG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1   MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQON
101 SPFSLKRNIG DLIPIAESS NINYQNFFQV GSALIFOYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

              70      80      90      100      110      120
m247-1.pep    NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQONSPPFSLKRNGIDK-LIPIAESSNI
              | : | : | | | | | : | : | | | | | : |
g247-1        PGAKQENPLFSLKRSGMDKQLIPVAESIDI
              10      20      30

              130      140      150      160      170      180
m247-1.pep    NYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK
              : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
g247-1        KYPGFIQRLNALVFQYGIDDLASAETVVVSSCSKIAPGKKISTLQEAKSALQITNDDK
              40      50      60      70      80      90

              190      200      210      220      230      240
m247-1.pep    EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVS
              | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
g247-1        -QNGNITROKHVVNAYAVGRFGNNEESLFRFQLDDKGKGNPQLLVKKVRMDVRYIYVS
              100      110      120      130      140

              250      260      270      280      290      300
m247-1.pep    GCPEDDDAGKEETFKYTDKFDSDAQNNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
              | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
g247-1        GCPEDDEDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLDSSLNAKIAASSDNSIYAYRINAT
              150      160      170      180      190      200

              310
m247-1.pep    IRGGNVCANRTLX
              | | | | |
g247-1        IRGGNVCANRTLX
              210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51 TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAA TGGAAATATC ACCCGTCAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCTTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTATATG TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pep (partial)..

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

              10      20      30
a247-1.pep    NNTAKLIPIAESTDIKYPGFAQARPALIFQ
              | : | | | | | : | : | : | : | : |
m247-1        GFGCFNMSEHPATDVIPDTTQONSPPFSLKRNGIDKLIPIAESSNINYNQNFFQVGSALIFQ
              80      90      100      110      120      130

              40      50      60      70      80      89
a247-1.pep    YGIDDLASAETVVVSSCSKIAPGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNA
              | | | | | : | | | | | : | | | | | : | : | | | | |
m247-1        YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNA
              140      150      160      170      180      190

              90      100      110      120      130      140      149
a247-1.pep    YAVGRIAGEEGLFRFQLDDKGKGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY
              | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```
m247-1      YAVGRIADEEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
              200           210           220           230           240           250

a247-1.pep   150           160           170           180           190           200
TGTFDSSSTNAVTPAGVEVLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
| | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m247-1      TDKFDQAQNAVTPAGVEVLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
              260           270           280           290           300           310
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

g248.seq

```
1 atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51 ggggtccgca ctgtttatcg tgctgatggg gatgatagtc gtggcctttt
101 tggttgtaac tgccgccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagc cggcttttgcg
201 ggaggcgcaa tttaggtttt tggatttggg atatctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaagggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgcctt gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgcgg caggcgctag caaaatgccg cgctatatta tcgaatattt
501 aggcgtgaag aacggacaaa atgtttatcg ggttactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgaaccaat aa
```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

g248.pep

1	MRKQNTLTGI	PTSDGQRGSA	<u>LFIVLMVMIV</u>	<u>VAFVLVVTAAQ</u>	SYNTEQRISA
51	NESDRKLALS	LAEAAALREGE	FQVLDLEYAA	DSKVTFSENC	EKGLCTAVNV
101	RTNNNGSEEA	FGNIVVQGKP	AVEAVKRSCP	AKSGKNSTDL	CIDNKGMEYN
151	KGAAGVSKMP	RYIIIEYLGVK	NGQNVYRVTA	KAWGKNANTV	VVLQSYVGNN
201	DEQ*				

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 961>:

```
m248.seq (partial)
1 ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.Tywt
51 gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAgTkCCA
101 ACgAAATCAGa CAGGAAATtG GCTwTGTCTT TGGCCGAGkG GkCTwTGCGG
151 GAAGGCGAAc TTCAGGTTtT GGATttGGAA tATGATACGg ACAGtAAGgT
201 TACATTTAGc GAAAACtGTG GAAAAGgCTG GTsTGCCGCA tGTAATGTGC
251 GGACAAATAa TGATAATGAA GAGGCTTTtG ACAATATCGT GGTGCAAGGC
301 AAGCCCAcCG TTGAGGCGGT GAAGCGTTtCT TGCCCTGCAa ATTCTACCGa
351 CCTGTGCATT GACAAgAAAG GgwtGGAATa TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAt ATTTGGGCGT GwAGAACGGA
451 GAAAATgTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGa ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAAGCAa TAATGATGAG TAA
```

This corresponds to the amino acid sequence <SEO ID 962; ORF 248>:

m248.pep (partial)

1	..GFALLIVLMV	XIVVAFXXVT	AAQSYNTEQR	ISXNESDRKL	AXSLAEXXXR
51	EGELQVLDLE	YDTSKVTFS	ENCGKGLXAA	VNVRTNNDNE	EAFDNIVVQG
101	KPTVEAVKRS	CPANSTDLCI	DKKGXEYKKG	TRSVTKMPRY	IIEYLGXVNG
151	ENVYRVTAKA	WKGKNTNVVV	LOSYYVNNDE	*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/q248

```

                                10      20      30      40
m248.pep      GFALLIVLMVXIIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
                | | | : | | | | | | | | | | | | | | | | | |

```


571

```

g248      MRKQNTLTGIPTSDGQGRGSALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCCKGLXAAVNVRTNND-NEEAFDNIVVQKGP
           50      60      70      80      90      100
           |||  |||:||||| :||||||| ||| :||||||| : ||| |||||
g248      LAEAAALREGEFQVLDLEYAADS KVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQKGP
           70      80      90      100     110     120

m248.pep  TVEAVKRSCPA---NSTDLCKKGXEYKKGTRSVTKMPRYII EYLVGXNGENVYRVTA
           110     120     130     140     150
           :||||||| |||||:| ||:|: :|:||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCKDKGMEYKNGAAGVSKMPRYII EYLVGXNGQNVYRVTA
           130     140     150     160     170     180

m248.pep  KAWGKNANTVVVLQSYVSNNDEX
           160     170     180
           ||||| |||||: |||
g248      KAWGKNANTVVVLQSYVGNNDEQX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1   ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGCCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1   MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSC TA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLVGXNGENV YRVTA KAWGK NANTVVVLQS YVSNNDE*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep  GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
           10      20      30      40
           |||:||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      MRKQNTLTGIPTSDGQGRGFA LFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCCKGLXAAVNVRTNNDNEEAFDNIVVQKGP
           50      60      70      80      90      100
           |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEAAALREGEFQVLDLEYDTSKVTFSENCCKGLCTAVNVRTNNDNEEAFDNIVVQKGP
           70      80      90      100     110     120

m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLVGXNGENVYRVTA KAWGK
           110     120     130     140     150     160
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      VEAVKRSC TAKSTGLCIDNK GMEYKKGTS VSKMPRYIIE YLVGXNGENVYRVTA KAWGK
           130     140     150     160     170     180

m248.pep  NANTVVVLQSYVSNNDEX
           170     180

```

a248

|||||
NANTVVVLQSYVSNNDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1   ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTAG CGAAACTGT GGAAAAGGTC TGTGTGCCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCACCC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGCGGCG TGAAGAACGG
501 AGAAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1   MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCPA NSTDLCDKK GMEYKKGTRS
151 VSKMPRYIE YLGVKNGENV YRVTAKAWGK NANTVVVLQS YVSNNDE*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQGKPT					
g248	LAEALREGE FQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNDNEEAFDNIVVQGKPT					
	70	80	90	100	110	119
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA-----NSTDLCDKKGMEYKKGTRSVSKMPRYIEYLGVKNGENVYRVT					
g248	AVEAVKRSCPAKSGKNSTDLCDKNKGMEYKGAAGVSKMPRYIEYLGVKNGQNVYRVT					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNNDEX					
g248	KAWGKNANTVVVLQSYVGNDEQX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQGKPT					
a248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCTAVNVRTNNDNEEAFDNIVVQGKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCDKKGMEYKKGTRSVSKMPRYIEYLGVKNGENVYRVTAKAWGK					
a248	VEAVKRSCAKSTGLCDKNKGMEYKKGTSVSKMPRYIEYLGVKNGENVYRVTAKAWGK					
	130	140	150	160	170	180

```

              190
m248-1.pep  NANTVVVLQSYVSNNDX
              |||||
a248         NANTVVVLQSYVSNNDX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```
g249.seq
1  atgaagaata atgattgctt ggcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgctgtc cgtacagtct cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca ttcgtcagcca aatcacgcaa aacctgatgg aaggaaatgtt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagctctt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtgct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcgga
601 ggtcgtgaat ga
```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

g249.pep

1	MKNNDCLRLK	NPQSGMALIE	<u>VLVAMLVLT</u> I	<u>GILALLSVQ</u> L	RTVASVREAE
51	TQTIVSQITQ	NLMEGMLMNP	TIDLDSNKKN	YSLYMGKQTL	SAVDGEFMLD
101	AEKSKAQLAE	EQLKRFSHEL	KNALPDAVAI	HYAVCKDSSG	DAPTLSDSGA
151	FSSNCDNKAN	GDTLIKVLWV	NDSAGDSDIS	RTNLEVSGDN	IVYTYQARVG
201	GRE*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```
m249.seq
1 ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51 GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CCGACAGCTN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATT TCGGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCCGA TATTTCCCGT ACCAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601 CGGGAATGA
```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```
m249 . pep
      1  MKNNDCFRLK  DSQSGMALIE  VLVAMLVLTI  GILALLSVQL  RTVXXXXXXXX
     51  XXXXXXXXXXXX  XLMEGMLMNP  TIDSDSNKKN  YNLYMGNHTL  SAVDGDFAID
    101  AMKTKGQLAE  AQLKRFSYEL  KNALPDAAAI  HYAVCKDSSG  NAPTLSGNAF
    151  SSNCNDKANG  DTLIKVLWVN  DSAGSDSISR  TNLEVSGDNI  VYTYQARVGG
    201  RE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

m249.pep MKQNDCFR LKDSQS GMALIEVL VAMLVLTIG ILALLSVQL RTVXXXXXXXXXXXXXXXXXXXX
| | | : | : | | | | | | | | | | | | | | | | | | | | | : | : |

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKGQLAEALKRFSYEL
           70      80      90      100     110     120
g249      NLMEGMLMNPTIDLDSNKKNYSLYMGKQ-TLSAVDGEFMDAEKSKAQLAEELKRFSHEL
           70      80      90      100     110     120
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND-SAGDS-
           130     140     150     160     170     179
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND-SAGDS-
           130     140     150     160     170     180
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           180     190     200
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCACTTG CGGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAATAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGGCCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTCGTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1   MKNNDCFRLK NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND-SAGDS- DI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
           10      20      30      40      50      60
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTKGQLAEALKRFSYE
           70      80      90      100     110     119
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNH-HALSVDGDFQVDAIKTKTQLAEALKRFSYE
           70      80      90      100     110     120
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND-SAGDS-
           120     130     140     150     160     170
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND-SAGDS-
           130     140     150     160     170     180

```

575

```

          180      190      200
m249.pep  SRTNLEVSGDNIVYTYQARVGGREX
          :|||||:|:|||||
a249      ARTNLETNGNNIVYTYQARVGGREX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 973>:

m249-1.seq

```

1  ATGAAGAATA ATGATTGCTT CCGCTGAAA GATTCCCACT CCGGTATGGC
51  GCTGATAGAA GTCTTGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CGGACAGTCG CTTCCGTCAG GGAGGCGGAG
151 ACACAAACCA TCGTCAGCCA AATCACGCAA AACCTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTTCGGCAG GGGATTCCGA TATTTCCCGT ACGAATCTTG
551 AGGTGAGCGG GCACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 974; ORF 249-1>:

m249-1.pep

```

1  MKNNDCFRLK DSQSGMALIE VLVAMLVLT GILALLSVQL RTVASVREAE
51  TQITVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHTL SAVDGDFAID
101 AMKTKQLAE AQLKRFSYEL KNALPDAAI HYAVCKDSSG NAPTLSGNAP
151 SSNCDNKANG DTLIKVLWVN DSAGSDISR TNLEVSGDNI VITYQARVGG
201 RE*

```

m249-1/g249 90.1% identity in 203 aa overlap

```

          10      20      30      40      50      60
m249-1.pep MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          |||||:|:|||||
g249       MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m249-1.pep NLMEGMLMNP TIDSDSNKKN YNLYMGNHTL SAVDGDFAIDAMKTKQLAE AQLKRFSYEL
          |||||:|:|||||:|:|||||:|:|||||:|:|||||
g249       NLMEGMLMNP TIDSDSNKKN YNLYMGNHTL SAVDGDFAIDAMKTKQLAE AQLKRFSYEL
          70      80      90      100     110     120

          130     140     150     160     170     179
m249-1.pep KNALPDAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGSDISR
          |||||:|:|||||:|:|||||:|:|||||:|:|||||
g249       KNALPDAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND SAGSDISR
          130     140     150     160     170     180

          180     190     200
m249-1.pep RTNLEVSGDNIVYTYQARVGGREX
          |||||:|:|||||
g249       RTNLEVSGDNIVYTYQARVGGREX
          190     200

```

a249/ L36117

gi|643582 (L36117) prepilin leader sequence requires cleavage to be active [Pseudomonas aeruginosa]
 >gi|1161222 (L48934) involved in type 4 fimbrial biogenesis; contains pre-pilin like leader sequence [Pseudomonas aeruginosa]
 >gi|1246299 (L76605) reference L36117, L48934 [Pseudomonas aeruginosa] Length = 185
 Score = 50.4 bits (118), Expect = 9e-06
 Identities = 45/183 (24%), Positives = 84/183 (45%), Gaps = 26/183 (14%)

```

Query: 13  QSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQNLMEGMLMNP 72
          QSG ++IEVLVA+L+++IG+L ++++Q +T+ ++ + + + NL+E M +P
Sbjct: 12  QSGFSMIEVLVALLISIGVLGMIAMQGKTIQYTADSVERNKAAMLGSLNLES MRASPKA 71

Query: 73  DSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKQLAE---QLKRFSYELKNALPDAA 129

```

Sbjct: 72 D + M G A + T L +A +L ++ ++KN LP A
 LYDVKDQ-----MATQSDFFKAKGSAFPTAPSSCTPLPDIAIKDRLGCVAEQVKNELPGAG 126

Query: 130 AI---HYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTL-IKVLWVND SAGDS DIARTNL 185
 + Y +C+ S +CDG G L I++ W + A ++

Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSML EIRLAWRGKQGACVNAADSSA 172

Query: 186 ETN 188
 +T+

Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAE	TQ			
a249	MKNND	CFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAE	TQ			
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLM	EGMLMNP	TIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAE	AQLKRFSYE		
a249	NLM	EGMLMNP	TIDSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKQLAE	AQLKRFSYE		
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNALPD	AAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND	SAGDS			
a249	LKNALPD	AAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND	SAGDS			
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTN	LEVSGDNIVYTYQARVGGREX				
a249	ARTN	LETNGNNIVYTYQARVGGREX				
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1   atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51  aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcagggcgg gcaaaaaggt atgggccggc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacgggtc acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcgccatat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga

```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1   MHTASPRDE FIRIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1   ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51  CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAACTACT CGGTATGCAG
101 GCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCACTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCACCTG TGGGCsGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCCTCG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA

```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1   MHTPSPHNEF IRGIKESPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51  MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*

```


g251.ppe

1	<u>MPDP</u> <u>I</u> <u>G</u> <u>I</u> <u>L</u> <u>F</u> <u>A</u>	<u>AVG</u> <u>V</u> <u>D</u> <u>F</u> <u>F</u> <u>A</u> <u>V</u>	<u>LR</u> <u>G</u> <u>R</u> <u>F</u> <u>Q</u> <u>R</u> <u>I</u> <u>G</u> <u>A</u>	<u>V</u> <u>G</u> <u>M</u> <u>L</u> <u>I</u> <u>I</u> <u>I</u> <u>I</u> <u>L</u>	<u>A</u> <u>E</u> <u>V</u> <u>G</u> <u>T</u> <u>K</u> <u>T</u> <u>V</u> <u>T</u>
51	<u>EV</u> <u>D</u> <u>A</u> <u>Q</u> <u>V</u> <u>V</u> <u>A</u> <u>D</u> <u>F</u>	<u>G</u> <u>G</u> <u>I</u> <u>E</u> <u>G</u> <u>F</u> <u>F</u> <u>E</u> <u>C</u> <u>R</u>	<u>L</u> <u>Q</u> <u>E</u> <u>P</u> <u>V</u> <u>A</u> <u>F</u> <u>P</u> <u>V</u> <u>N</u>	<u>H</u> <u>A</u> <u>V</u> <u>G</u> <u>F</u> <u>V</u> <u>V</u> <u>G</u> <u>R</u> <u>R</u>	<u>L</u> <u>V</u> <u>G</u> <u>T</u> <u>R</u> <u>A</u> <u>A</u> <u>I</u> <u>F</u> <u>V</u>
101	<u>R</u> <u>T</u> <u>V</u> <u>G</u> <u>G</u> <u>T</u> <u>V</u> <u>R</u> <u>L</u>	<u>K</u> <u>M</u> <u>I</u> <u>V</u> <u>Q</u> <u>T</u> <u>D</u> <u>A</u> <u>L</u> <u>P</u>	<u>V</u> <u>V</u> <u>R</u> <u>E</u> <u>A</u> <u>G</u> <u>I</u> <u>I</u> <u>R</u> <u>P</u>	<u>S</u> <u>V</u> <u>F</u> <u>I</u> <u>G</u> <u>I</u> <u>G</u> <u>I</u> <u>D</u>	<u>F</u> <u>Q</u> <u>T</u> <u>V</u> <u>A</u> <u>A</u> <u>F</u> <u>G</u> <u>V</u> <u>R</u>
151	<u>L</u> <u>V</u> <u>V</u> <u>K</u> <u>H</u> <u>A</u> <u>R</u> <u>T</u> <u>V</u>	<u>R</u> <u>A</u> <u>H</u> <u>L</u> <u>R</u> <u>T</u> <u>V</u> <u>T</u> <u>F</u>	<u>G</u> <u>N</u> <u>Q</u> <u>P</u> <u>A</u> <u>V</u> <u>F</u> <u>A</u> <u>R</u> <u>P</u>	<u>S</u> <u>R</u> <u>F</u> <u>A</u> <u>V</u> <u>A</u> <u>S</u> <u>Y</u> <u>D</u>	<u>V</u> <u>F</u> <u>F</u> <u>I</u> <u>F</u> <u>I</u> <u>K</u> <u>N</u> <u>R</u> <u>L</u>
201	<u>G</u> <u>Q</u> <u>E</u> <u>C</u> <u>R</u> <u>N</u> <u>R</u> <u>H</u> <u>I</u> <u>A</u>	<u>R</u> <u>V</u> <u>E</u> <u>S</u> <u>L</u> <u>L</u> <u>R</u> <u>A</u> <u>F</u> <u>E</u>	<u>Y</u> <u>A</u> <u>A</u> <u>D</u> <u>V</u> <u>V</u> <u>P</u> <u>F</u> <u>V</u>	<u>K</u> <u>T</u> <u>K</u> <u>T</u> <u>R</u> <u>A</u> <u>E</u> <u>O</u> <u>P</u> <u>R</u>	<u>P</u> <u>A</u> <u>F</u> <u>V</u> <u>*</u>

m251.seq

1	ATGCGTGTCTG	CGGTAGTCGT	AGCGCAAGCC	CGCGCCGACA	TCCGCCACC
51	TGCCCCAAACG	GACATTGTCC	CGAACTGCCG	CGTAATAGCT	TTTACCGTTG
101	ATGCTGCGCG	GCGTGCAGTC	CGTATAAGTA	TTGTTGCCCA	AGCGGCAGAT
151	TTGCCCCGTA	ACGACATTTT	CCCTGCCTAT	GGTGACCCAA	TAGGGGCTGG
201	TTTCACTGCC	GTTGGGGCTG	ATTTTTTTGC	CGTTGTTTTG	AGGGGGCGTG
251	TTTCAGCAAT	AGGCGCGGTT	GGCATGTGA	TAATAATAAT	CCTGATGGCG
301	GAGATTAGAG	CCAAAGCGGT	CAAAACCCG	ATTACAGCTC	AGGTTGTGGC
351	GGATTTTGGC	GGTATCGAAG	GATTTTTTGA	ATGCCGCTG	CAAGACGCTG
401	TGGCTTTCCC	CGTAAATCAC	GCGATCGGAT	TTGTAATAGG	AAAACGGCTT
451	GTCGGCACTC	GGGCGGCAAT	ATTTGTCCGA	ACCGTCGGCA	GAACAGTGCG
501	TCTGCTGAAA	ATGATTATCC	AAACCGATCG	CCTGCCGGTC	GTAAGAGAGG
551	CGGGCATAAT	CCGCCCAAGT	GTCTTTATCG	GCATTGGTAT	AGACATATTC
601	CAAACCGTAG	CGGCTTTTGG	TGTGCGTCTC	GTCGTAAAAC	ACGCCCGTAC
651	CGTATTCCGC	GCCCACCAGC	GCACCGTTTT	CGCCGTTGGT	AAACAGTCCG
701	CCGTATTTGT	GGTTGCCCGC	GTATTTGCCG	TTACCGGGCA	AAGAACC CGC
751	CTGTTTTTTA	TTTGCATCAA	AAACCGCCTT	GGTCAGGAAT	GCCGGAACCG
801	TCATATCGCG	CGTGTCGAAA	GTTTGTTCGG	TGTGTTGAG	TATGCCGCCG
851	ATGTAGTGCC	GCTTATTCTC	AAAACGAAAA	CCCGGGCGGA	ACAGCCACGA
901	CCGGCTTTCC	TATGA			

m251.ppt

1	MRAAVVVAQA	RADIRPPAQT	DIVPNCRVIA	FTVDAARRAV	RISIVAQAAD
51	LPRNDISPAY	GDPIGAGFTA	VGADFFFAVL	RGRVRRIGAV	GMLIIILMA
101	EIRAKAVKPE	IHAQVVADEG	GIEGFFECRL	QEPVAFFPNH	AIGFVIGKRL
151	VGTRAAIFVR	TVGRTVRLLK	MIQTDALPV	VREAGIIRPS	VFIGIGIDIF
201	QTVAAFGVRL	VVKHARTVFR	AHQRTVFAVG	KQSAVFVVAR	VFAVTGQTR
251	LFACIKNRL	GQECRNRHIA	RVESLLRVFE	YAADVPLIL	KKTKTRAEQPR
301	PFFIV*				

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

40 50 60 70 80 90
 m251.pep TVDAARRAVRISIVAQAADLPNRNDISPAYGDPFIGAGFTAVGADFFAVVLRGRVRRIGAVG
 ||||| :|||:||||| :|||
 g251 MPDPFIGILFAAVGVDFFAVVLRGRFRQIRAVG
 10 20 30

579

	100	110	120	130	140	150
m251.pep	MLIIIIILMAEIRAKAVKPEIHAQVVADFGGIEGFFECRLQEPVAFPNHAI GFVIGKRLV					
g251	MLIIIIILMAEVGKT VVTEVDAQVVADFGGIEGFFECRLQEPVAFPNH AVGFVVGRRLV					
	40	50	60	70	80	90
	160	170	180	190	200	210
m251.pep	GTRAAIFVRTVGR TVRLLKMI IQTDALPVVREAGIIRPSVFIGIGIDIFQTVA AFGVRLV					
g251	GTRAAIFVRTVGGTVRLLKMIVQTDALPVVREAGIIRPSVFIGIGIDIFQTVA AFGVRLV					
	100	110	120	130	140	150
	220	230	240	250	260	270
m251.pep	VKHARTVFRAHQRTVFAVGKQSAVFVVARVFAVTGQTRLFFICIKNRLGQECRN RHIA R					
g251	VKHARTVFRAHLRTVFTVGNQPAVFAAARVFAVASYRS-VFFIFIKNRLGQECRN RHIA R					
	160	170	180	190	200	210
	280	290	300			
m251.pep	VESLLRVFEYAADV VPLILKTKTRAEQPRPAFVX					
g251	VESLLRAFEYAADV VPFVFKTKTRAEQPRPAFVX					
	220	230	240			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 985>:

```

a251.seq
1   ATGCGTGCTG CGGTAGTCGT AGCGCAACCC CGCGCCGACA TCCGCCACCC
51  TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTGCCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACCACATTTC CCCTGCCTAT GCTGACCCAA TAGGGTTGGT
201 CCTTGCCGCC GTTGGGGTTG GCGGTTTTAG GGGGCGTTTT CGACGAATAG
251 GCGCGGTTGG CATGTTGATA ATAATAATCC TGATGGCGGA GATTAGAGTC
301 AAAGCGGTCA AAACCGAGAT TCACGCTCAG GTTGTGGCGG ATTTTGGCGG
351 TATCGAAGGA TTTTGTGAAT GCCGCTGCA AGAGCCTGTG GCTTTCCTCG
401 TAAATCACGC GGTCCGATTT GTAGTAGGAA AACGGCTTGT CGGCACTCGG
451 GCGGCAATAT TTGTCCGAAC CGTCGGCAGA ACAGTGCCTC TGCTGAAAT
501 GATTGTCCAA ACCGATGCCC TGCCGGTCGT AAGAGAGGCG GGCATAATCC
551 ACCCAAGTGT CTTTATCGGC ATTGGTATAG ACATATTCCA AACCGTAGCG
601 GCTTTTGGTG TCGCTCTCGT CGTAAACAC GCCCGTACCG TATTCCGCGC
651 CCACCAGCGC ACCGTTTTCG CCGTTGGTAA ACAGACCGCC GTATTTGTGG
701 TCGCCCGCGT ATTTGCCGTT GCCTCTATC GGTCCGTATT TTCTATTTTC
751 ATCAAAAACC GCCTTGGTCA GGAATGCCG AACCCTCATA TCGCGCGTGT
801 CGAAAGTTT TCGCGTGTGT TCGAGTATG CGCCGATGTA GTGCCGTTT
851 TTTTCAAAC GAAAACCCG GCGGAACAG CACGATCGG TTTCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 986; ORF 251.a>:

```

a251.pep
1   MRAAVVVAQP RADIRPPAQT DIVPNCRVIA FAVDAARRAV RISIVAQAAD
51  LPRNHISPAY ADPIGLVLAA VGVGGFRGRF RRIGAVGMLI IILMAEIRV
101 KAVKTEIHAQ VVADFGGIEG FFECRLQEPV AFPVNHAVGF VVGKRLVGR
151 AAIFVRTVGR TVRLLKMIVQ TDALPVVREA GIIHPSVFIG IGIDIFQTV
201 AFGVRLVVKH ARTVFRAHQRT VFAVGKQTA VFVVARVFAV ASYRSVFSIF
251 IKNRLGQECR NRHIA RVESL LRVFEYAADV VPFVFKTKTR AEQPRSAFV*

```

m251/a251 88.5% identity in 304 aa overlap

	10	20	30	40	50	60
m251.pep	MRAAVVVAQARADIRPPAQT DIVPNCRVIAFTVDAARRAVRISIVAQAADLPRNDISPAY					
a251	MRAAVVVAQPRADIRPPAQT DIVPNCRVIAFAVDAARRAVRISIVAQAADLPRNHISPAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m251.pep	GDPIGAGFTAVGADFFAVVLRGRVRRIGAVGMLIIIIILMAEIRAKAVKPEIHAQVVADFG					
	: : : :					

580

```

a251      ADPIGLVLAAVGVGGF----RGRFRIRGAVGMIIIIILMAEIRVKAVKTEIHAQVVADFQ
              70          80          90          100         110

m251.pep      130          140          150          160          170          180
GIEGFFECLRLQEPVAFPVNHAIGFVIGKRLVGTRAAIFVRTVGRVTVRLLKMIIQTDALPV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECLRLQEPVAFPVNHAVGFVVGKRLVGTRAAIFVRTVGRVTVRLLKMIVQTDALPV
              120          130          140          150          160          170

m251.pep      190          200          210          220          230          240
VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQSASFVVAR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQTAFFVVAR
              180          190          200          210          220          230

m251.pep      250          260          270          280          290          300
VFAVTGQRTLRFICIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTAEQPR
|||::|:|:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VFASVSYS-RFSIFKNRLGQECRNRIARVESLLRVFEYAADVPFVFKTKTAEQPR
              240          250          260          270          280          290

m251.pep      PAFVX
               |||
a251      SAFVX
               300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

g253 . seq

```
1 atgatcgaca gggaccgtat gttgcgggac acgttggaac gtgtgcgtgc
51 ggggtcgttc tggttatggg tgggtggtggc atcgatgatg tttaccgcgc
101 gattttcagg cacttatctt ctgatggaca atcaggggct gaatttcott
151 ttagttttgg cgggagtggt gggcatgaat acgtgatgc tggcagtatg
201 gttggcaacg tctgtctctg gcgtgaaagt gggacggttt ttcagcagtc
251 cggcgacgtg gtttcggggc aaagggcctg taaatcaggc ggtgtgctcg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttctggc tctgcacgct gctcggaatg ctggtgtcgg
401 tattgctgct gcttttgggt cggcaatata cgttcaactg ggaaagcacg
451 ctggtgagca atgcgcgttc ggtacgcgcg gtggaaatgt tggcatggct
501 gccgtcgaaa ctcggtttcc ctgtcccgca tgcgcgggct gtcatcgaag
551 gtcgtctgaa cggcaatatt gccgatgcgc gggcttggtc ggggctgctg
601 gtcggcagta tctgtctgcta cggcatcctg ccgcgcctct tggcttgggt
651 agtgtgtaaa atccttttga aaacaagcga aaacggattg gatttggaaa
701 aaacctatta tcaggcggtc atccgcgcgt ggcagaacaa aatcaccgat
751 gcgatacgc gtcgggaaac cgtgtccgcc gtttcgccga aaatcgtctt
801 gaacgatgcg cgcgaatatg gctctatgct ggagaccgag tggcaggacg
851 gccaatgggt cgagggcagg ctggcgcgag aatggctgga taagggcgtt
901 gccgccaatc gggaacaggt tgccgcgcgt gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaactgtg ccggaccggg
1001 gcgtgctgcg gcagatttgt cggctttcgg aagcggcgca gggcggcgcg
1051 gtggtctcag ttttggcgga acaggggctt tcagcagacc tctcggaaaa
1101 gctggaacat tggcgtaacg cgctgaccga atcgggcgcg gcgtggcttg
1151 agcctgacag ggtggcgcac gaaggccggt tgaagaacca ataa
```

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253.pep

1	MIDRDRMLRD	TLERVAGSF	WLWVVVASMM	FTAGFSGTYL	LMDNQGLNFF
51	LVLAVGLGMN	TLMLAVLAT	LFLRVKVGRF	FSSPATWFRG	KGPVNQAVLR
101	LYADQWRQPS	VRWKIGATAH	SLWLCTLLGM	LVSVLLLLLV	ROYTFNWEST
151	LLSNAASVRA	VEMLAWLPSP	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
201	VGSIVCYGIL	PRLLAWVCK	ILLKTSENGL	DLEKTYQQAV	IRRWNQNKTD
251	ADTRRETVSA	VSPKIVLNDA	PKWALMLETE	WQDQWFEGR	LAEWLKDKVD

301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRLQIV RLSEAAQGGGA
 351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRVAQ EGRLKDQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

m253.seq
 1 ATGATTGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
 51 GGGGTCGTTC TGGTTGTGGG TGGTGGCGGC GACGTTTGCA TTTTATACCG
 101 GTTTTTCAGT CACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
 151 TTGGTTTGG CCGGCGTGT TGGCATGAAT ACGCTGATGC TGGCAGTATG
 201 GTTGGCAATG TTGTTCCCTGC GTGTGAAAGT GGGGCGTTTT TTCAAGCAGTC
 251 CGGCGACGTG GTTTCGGGGC AAAGACCCTG TAAATCAGGC GGTGTTGCGG
 301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
 351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGTTGTCGG
 401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCACG
 451 CTGTTGAGCA ATGCCGCTTC GGTACGCGCG GTGGAATGT TGGCATGGCT
 501 GCCGTCGAAA CTCGGTTTTCC CTGTCCCCGA TCGCGGGGCG GTCATCGAAG
 551 GCCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGGTC GGGGCTGCTG
 601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTGC TGGCTTGGGT
 651 AGTGTGTAAG ATCCTTTTGA AAACAAGCGA AAACGGATTG GATTGGGAAA
 701 AGCCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCGAT
 751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCACCGA AAATCATCTT
 801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAG TGGCAGGACG
 851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
 901 GCCACCAATC GGGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
 951 ACCGCGCAA CTGCTTATCG GCGTGCAGCG CCAAACGTG CCGGACCGCG
 1001 GCGTGTGCG GCAGATTGTC CGACTCTCGG AAGCGGCGCA GGGCGGCGCG
 1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGAAAAA
 1101 GCTGGAACAT TGGCGTAACG CGCTGGCCGA ATGCGGCGCG GCGTGGCTTG
 1151 AGCCTGACAG GCGGCGCAG GAAGGGCGTT TGAAAGACCA ATAA

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pep
 1 MIDRNRMLRE TLERVAGSF WLWVVAATFA FFTGFSVTYL LMDNQGLNFF
 51 LVLAGVLGMN TLMLAVLAM LFLRVKVGFR FSSPATWFRG KDPVNQAVLR
 101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLLV RQYTFNWEST
 151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRNLNGNI ADARAWSGLL
 201 VGSIACYGIL PRLLAWVCK ILLKTSENGL DLEKPYQAV IRRWQNKITD
 251 ADTRRETQSA VSPKILNDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
 301 ATNREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRLQIV RLSEAAQGGGA
 351 VVQLLAEQGL SDDLSEKLEH WRNALAECGA AWLEPDRAAQ EGRLKDQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

m253.pep	10	20	30	40	50	60
	MIDRNRMLRETTLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAVLGMN					
g253	MIDRDRMLRDTTLERVAGSFWLWVVVASMFTAGFSGTLYLLMDNQGLNFFLVLAVLGMN					
	10	20	30	40	50	60
m253.pep	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGRRFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGRRFSSPATWFRGKGPVNQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
m253.pep	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRVEMLAWLPSKLGFPVPDARA					
g253	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180

	190	200	210	220	230	240
m253.pep	VIEGRLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
	:					
g253	VIEGRLNGNIADARAWSGLLVGSIVCYGILPRLLAWVVKILLKTSENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETVSASP K I LNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	:					
g253	IRRWQNKITDADTRRETVSASP K I V LNDAPKWALMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGA VVQLLAEQGL					
	:					
g253	AANREQVAALETELKQKPAQLLIGVRAQTV PDRGVLRQIVRLSEAAQGGA VVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
	:					
g253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKDQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a253.seq
1  ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTTT TGGTTGTGGG TGGCGGCGGC GACGTTTGCG TTTTACCCTG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGGTTTGGG CGGGCGTGTT GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGAATG TTGTTCTGTC GCGTGAAGT GGGGCGTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTCCG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCAGC
451 CTGTTGGGCG ATTCGTCTTC GGTACGGCTG GTGGAAATGT TGGCATGGCT
501 GCCTGCGAAA CTGGGTTTTT CCGTGCCTGA TCGCGCGGCG GTCATCGAAG
551 GTCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGCTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGGGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTGGAAGA
701 AGCCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCAGT
751 GCGGATACGC GTCGGGAAAC CGTGTCGCC GTTTCGCCGA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
901 GCCGCCAATC GGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGC GCGC CCAACTGTG CCCGACCGCG
1001 GCGTGTTCG GCAGATCGTC CGACTTTCG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTCGGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG GCGTGGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGAAAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a253.pep
1  MIDRNRMLRE TLERVRAGSF WLWVAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVWLAM LFLRVKVRG FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLLV RQYTFNWEST
151 LLGDSSSVRL VEMLAWLPAK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
201 VGSIIACYGIL PRLLAWAVCK ILLKTSENGL DLEKPYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIVLNDK PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGA
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAAQ EGRLKTNDR
401 *

```

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
a253	MIDRNRMLRETLERVAGSFWLWVAAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFLRVKVGRRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWVVKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWAVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253.pep	IRRWQNKITDADTRRETSAVSPKIIINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWQNKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253.pep	ATNREQVAALETELKQKPAQLLIGVRAQTPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVAALETELKQKPAQLLIGVRAQTPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcaggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggcccgggc
301 tggacggtat tttcactgtc ctggctgctg gcggctgcag gaatcgacac
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggctcttg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSLT
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
 201 VSVYGYVI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
 51 GTACCACGGA ATTGCAGCCG GAAAACCTGAA AAGCATTTTG AAAAAACCG
 101 ACCACTGCAT GATTATATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATT ATGTCGTCAT GGGTTGGATG
 301 GTCTTGCGCG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
 351 GGCTTGCGTG GCGGCAGGCG GTATGCTGTA CAGTGTGGCG ATTTACTGGT
 401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC
 451 GTATTGGGCG GCAGCATCAC CCAATTGTG AGCGTGTACG GTTACGTAAT
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI KKTDHCMYI VLIAGSYTPFA
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLLS IYIYVVMGWM
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF
 151 VLGGSTQFV SVYGYVI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGLMLMLLKTIGHGDYRIFSVSVYGISLLL	LYLSSSLYHG	IAAGKLKSI			
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAGIAQELTI
g254		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPGW	TVFSLSWLLA	AAGIAQELTI
		80	90	100	110	120
m254.pep		100	110	120	130	140
		IYIYVVMGWM	VLAVMKSLTA	SLPSAGLAWL	AAGGMLYSVG	IYWFVNDEKI
g254		IAIYIVMGWM	VLAVMKSLTA	SLPPAGLAWL	AAGGMLYSVG	IYWFVNDEKI
		140	150	160	170	180
m254.pep		160				
		VLGGSTQFV	SVYGYVIX			
g254		VLGGSTQFV	SVYGYVIX			
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTTGA GCGGTTTGAT
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
 151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAT CCGGAAAACCT
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

1	<u>MYTGERFNTY</u>	<u>SHLSGLILAA</u>	<u>AGLALMLLKT</u>	<u>IGHGDGYRIF</u>	<u>SVSVYGISLL</u>
51	<u>LLYLSSSLYH</u>	<u>GIAAGKLKSI</u>	<u>LKKTDHCMYI</u>	<u>VLIAGSYTPF</u>	<u>ALVSLRNGPG</u>
101	<u>WTVFSLSWLL</u>	<u>AAAGIAQELT</u>	<u>IGRKSEKRL</u>	<u>SLAIYIVMGW</u>	<u>MVLAVMKSIT</u>
151	<u>ASLPAGLAW</u>	<u>LAAGGMLYSV</u>	<u>GIYWFVNDEK</u>	<u>IRHGHIWHL</u>	<u>FVLGGSITQF</u>
201	VSVYGYVI*				

```

30                                     10                                     20
m254.pep
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL
|||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL
20          30          40          50          60
70
40          50          60          70          80
90
m254.pep
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
80          90          100          110          120
130
100          110          120          130          140
150
m254.pep
IVIYVVMGWMVLAVMKSLTASLPSAGLAWLAAGGMLYSVGIYWVFVNDEKIRHGHGIWHLF
|:|:|||||
a254
IAIYIVMGWMVLAVMKSLTASLPPAGLAWLAAGGMLYSVGIYWVFVNDEKIRHGHGIWHLF
140          150          160          170          180
190
160
m254.pep
VLGGSITQFVSVYGYVIX
|||||
a254
VLGGSITQFVSVYGYVIX
200

```

BNSDOCID: <WO__9957280A2_1_>

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

g255 . pep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/q255

BNSDOCID: <WO 8957280A2 | >

587

	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```
a255.seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG TGTTTCGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCACG GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GGCGGTCGAA
151 TACGGGTTTCG CCCAAGCCGA CGGGGACGTT GGCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTTGCGCA CGCTGTCCAT ATAGTTTCC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTTCGCAG CCTTCAAACC GGATTTCTTT TTCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTTT TCAACCATT TTTGGCAACG
401 GCTCCGCGCG CAACGCGGGC GCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```
a255.pep
1   VVGQEALRGE FVAVFAAALR YAVKTCADFH AFDGVDAAHG VGDFGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG GGFAGGTPAA
151 APVVARAVFV FIGIVGVAGA EAGGDVAVVF AALVGIAD*
```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDVDFGIEAVKNRFAQADRD					
	:					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHGVGDVDFGIEAVEYGFAGADGDV					
	10	20	30	40	50	60
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD					
	:					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD					
	:					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFFQPFNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
a255	FRAEFFFQPFNGSGSNAGGGFAGGTPAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
m255.pep	FRAEFFFQPFNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
	:					
a255	FRAEFFFQPFNGSGSNAGGGFAGGTPAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```
g256.seq
1   atgctcgcgg tacgcaatcg gggttggcac ggcgcagtcg tccatttcgg
51  cagctgcggc ggcgtagcga acaccgcccc ggtgttctac cacttggggtg
101 ataccgccga aatcgctttt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251 ccgccccgtg tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggtcgc tctacacgcg ctacttcctc cgcacactga taccctaaagc
```

g256.pep

1	MLAVNRNRGWH	GAVVHFRSCG	GVANTAPVVFY	HLGDTAEIAF	ALDTLTARYR
51	EIYAVGVSLG	GNAPAKYLGE	QGKKALPHAS	AAVSAPVDAE	AAGSRFDSGI
101	TRLLYTRYFL	RTLIPKARSL	<u>QGFQTAFAAG</u>	CKTLGEFDDR	FTAPLHGFD
151	RHDYYRQTS	KPLLKHVAKP	LLLLNAANDP	FLPPEALPRA	DEASEAVTLF
201	QPAHGHHAGF	VSSTGGRHLH	QWLPQTVLSY	FDSFTRNRR*	

m256.seq

1	ATGCTTGCGG	TACGCGATCG	GGGTTGGCAC	GGCGTAGTCG	TCCATTTCGG
51	CAGCTGCGGC	GGCATTGCCA	ACACCGCTCC	GGTGTCTAC	CA. CTGGCG
101	ATACCGATCC	AATCGCCTTT	ACTTTGGACA	CGTTCGCCGC	GC GTTACCGT
151	GAAAcTACG	CCGTCCGGCT	ATCGCTGGGG	GGCAACCGCT	TGGCAAATA
201	TTTGGGCGAA	CAGGGCAAAA	AGGCATTGCC	GCAAGCCGCT	GCCGT CATCT
251	CCGCCCCCGT	CGATGCAGAG	CGCGCAGGCA	GACGTTCTGA	CACGGGCATC
301	ACGCGGCTGC	TCTACACGCG	CTACTTCCTC	CGCACCCTGA	TACCCAAAGC
351	AAAATCGCTC	CAAGGTTTTC	AGACGGCATT	TGCCCGAGGG	TGCAAAACAC
401	TGGCGCAGTT	TGACGACCCG	TTCACCGCGC	CGCTGCACGG	CTTTGCCGAC
451	CGGCACAGT	ACTACCGCCA	AACTTCCTGC	AAACCGCTGC	TCAAACACGT
501	TGCCAAACCG	CTGTCTCTGC	TCAATGCCGT	CAACGACCCC	TTCTGCCCGC
551	CCGAAGCCCT	GCCCCGCGCA	GACGAAGTAT	CCGAAGCCGT	TACCTGT TTC
601	CAGCCGGCAT	ATGGTGGTCA	TGTCTGGCTTT	GTCAGCAGCA	CCGGCGGCAG
651	GCTGCACCTG	CAATGGCTGC	CGCAGACCGT	CCTGTCCTAT	TTCGACAGCT
701	TCCGCACAAA	CAGGCGTTAA			

m256 . pep

```

1  MLAVRDRGWGH  GVVVHFRSCG  GIANTAPVIFY  XLGDTAEIAF  TLDTFAARYR
51  EIYAVGVSLG  GNALAKYLGE  QGKKALPQAA  AVISAPVDAE  AAGRFRDSGI
101  TRLLYTRYFL  RTLIPKAKSL  QGFQTAFAAG  CKTLGEFDDR  FTAPLHGFD
151  RHDYYRQTS  C  KPLLKHVAKP  LLLLNVDNDP  FLPEALPRA  DEVSEAVTLF
201  QPAYGGHVGF  VSSTGGRHLH  QWLPQTVLSY  FDSFRTNRR*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m256/g256

```

m256.pep      10      20      30      40      50      60
               MLAVRD1RGW2HGVV3HFR4SCGG5IANTAPV6FYHLG7DTAE8IAFT9LD10TFA11ARY12REI13YAV14GVSL15G
g256          10      20      30      40      50      60
               MLAVRN1RGW2HGAV3VHFR4SCGG5VANTAPV6FYHLG7DTAE8IAF9ALD10TLT11ARY12REI13YAV14GVSL15G

m256.pep      70      80      90      100     110     120
               GNALAKYLGEQGKKALPQAAAVISAPVDAEAAAGRRFD1SGITRL2LYTRY3FLRT4LIPKA5KS6L
g256          70      80      90      100     110     120
               GNAPAKYLGEQGKKALPHASA1AVSAPVDAEAAAGSRFD2SGITRL3LYTRY4FLRT5LIPKA6RS7L

m256.pep      130     140     150     160     170     180
               QGFQTAFAAGCKTLGEFDD1RF2TAPLHGFA3DRHD4YYRQ5TSC6KPLLKH7VAKPL8LLLLNA9VND10P
g256          130     140     150     160     170     180
               QGFQTAFAAGCKTLGEFDD1RF2TAPLHGFA3DRHD4YYRQ5TSC6KPLLKH7VAKPL8LLLLNA9AND10P

```

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

a256.seq

1	ATGCTCGCGG	TACGCGATCG	GGGTTGGAAC	GGCGTAGTCG	TCCATTTCCG
51	CAGCTGCGGC	GGCGTAGCGA	ACACCGCCCC	GGTGTCTAC	CACTTGGGCG
101	ATACCGCCGA	AATTGCCTTT	ACTTTGGACA	CGCTCGCCGC	GCGTTACCGT
151	GAAATATACG	CCGTCGGCGT	ATCGCTGGGC	GGCAACCGCG	TGGCAAATA
201	TTTGGGCGAA	CAGGGCGAAA	ACGCGCTGCC	GCAAGCCGCC	GCCGTCATCT
251	CCGCACCCGT	CGATGCAGAG	GCGGCAGGCA	ACCGCTTCGA	CAGCGGCATC
301	ACACGGCTGC	TCTACACGCG	CTACTTCCTC	CGCACACTGA	TACCCAAAGC
351	ACGGTCGCTC	CAAGGTTTTT	AGACGGCATT	TGCCGCAGGG	TGCAAAACAC
401	TGGGCGAGTT	TGACGACCGT	TTCACCGCAC	CGCTGCACGG	CTTTGCCGAT
451	CGGCACGACT	ACTACCGCCA	AACTTCCTGC	AAACCGCTGC	TCAAACACGT
501	TGCCAAACCG	CTGCTCCTGC	TCAATGCCGT	CAACGACCCC	TTCTTGCCGC
551	CCGAAGCGCT	GCCCCGCGCA	GACGAAGTGT	CCGAAGCCGT	TACCTGTTC
601	CAGCCGACAC	ACGGTGGTCA	TGTCGGCTTT	GTCGGCAGCA	CCGGCGCAG
651	GCTGCACCTG	CAATGGTTGC	CGCAGACCGT	CCTGTCTTAT	TTGCACAGCT
701	TCCGCACAAA	CAGGCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

a256.pep

1	MLAVRDRGWN	GVVVHFRSCG	GVANTAPVfy	HLGDTAEIAF	TLDTLAARYR
51	EIYAVGVSLG	GNALAKYLGE	QGENALPQAA	AVISAPVDAE	AAGNRFDSGI
101	TRLlyTRYFL	RTLIPKARSL	QGFQTAFAAG	CKTLGEFDDR	FTAPLHGfAD
151	RHDYyRQTSC	KPLLKHVAKP	LLLNAVNDP	FLPPEALPRA	DEVSEAVTLF
201	QPTHGGHVGf	VGSTGGRLHL	QWLPQTVLSY	FDSFRTNRR*	

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVfyXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNGVVVHFRSCGGVANTAPVfyHLGDTAEIAFTLDTLAARYREIYAVGVSEg					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQgKKALPQAAAVISAPVDAEAAGRRFDSGITRLlyTRYfLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGITRLlyTRYfLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGfADRHdYyRQTsCKPllKHVAKPllllNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGfADRHdYyRQTsCKPllKHVAKPllllNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGfVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGfVGSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

g256-1.seq

1	ATGATTTTGA	CACCGCCGGA	CACGCCCTTT	TTCCTCCGCA	ACGGCAATGC
51	CGACACGATT	GCCGCCAAT	TCCTGCAACA	CCCCGCACCC	GCATACCGCC

```
101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCGG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTCGAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GCGCGAGTCG TCCATTTCGG CAGCTGCGGC
301 GCGGTAGCGA ACACGCCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCCTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 GCCCGCTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTT CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```
1 MILTPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EYAVGVSLG GNAPAKYLGE
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD RHDYYRQTSK PLLKHVAKP
251 LLLNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRHLH
301 QWLPQTVLSY FDSFRTNRR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```
1 ATGATTTTAA CACCGCCGGA CAGGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCAGCGCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTGCCCCGA TGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCGAGC ATTACGCGGT CGAAGTATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCGC CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCGC
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAATATTT GGGCGAACAG
451 GGCAAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCGCCGTGTA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAG CCGCTGCTCT
551 ACACGCGCTA CTTCTCCGC ACCCTGATAC CCAAAGCAA ATCGCTCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGGTGC AAAACACTGG GCGAGTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCGGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CTTGTTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCCT GTCCTATTTC GACAGTTTCC GCACAAACAG
951 GCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```
1 MILTPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVDRGWHG VVVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVGFV SSTGGRHLHQ
301 WLPQTVLSYF DSFRTNRR*
```

m256-1/g256-1 93.1% identity in 319 aa overlap

```
10 20 30 40 50 59
m256-1.pep MILTPDTPFFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
|||||
g256-1 MILTPDTPFFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
10 20 30 40 50 60

60 70 80 90 100 110 119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVDRGWHGVVVHFRSCGGIANTAPVYFHLGDTAEIAF
```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1015>:

1	ATGATTTTGA	CACCGCCGGA	CACACCCTTT	TTCTCTCGCA	ACGGCAATGC
51	CGACACGATT	GCCGCCAAAT	TCCTGCAACG	CTCCGCACTC	GCATACCGCC
101	CGAGAGCTGCT	TCCCACGACG	ACGGGTAAAA	CCAAAACCCG	CTACGACTTT
151	TCAGACGGCA	TTTCGGCCGA	TCCGGCTGCG	GTCGTGCTGT	TTACCGGTTT
201	GGAGGGCGCG	AGTGGCAGCC	ATTACCGGGT	CGAACTGTATG	CTCGCGGTAC
251	GGCATCGGGG	TTGGAACGGC	GTAGTCGTCC	ATTTCGCGAC	CTCGCGGCGC
301	GTAGCGAACA	CCGCCCCGGT	GTTCTACAC	TTGGGCGATA	CCGCCGAAAT
351	TGCTCTTTAT	TTGGACACGC	TCGCCGCGCG	TTACCGTGAA	ATATACGCCG
401	TCGGCTGTATC	GCTGGGCGGC	AACGCGCTGG	CAAAATATTT	GGGCGAACAG
451	GGCGAAAACG	CGCTGCGCGA	AGCCGCCCTC	GTCATCTCCG	CACCCGTCGA
501	TGCAGAGGCG	GCAGGCAACC	GCTTCGACAG	CGGCATCACA	CGGCTGCTCT
551	ACACGCGCTA	CTTCTCTCCG	ACACTGATAC	CCAAAGCAGC	GTCGCTCCAA
601	GTTTTCAGA	CGGCATTTCG	CGCAGGGTGC	AAAACACTGG	CGGAGTTTGA
651	CGACCGTTTC	ACCCACCCGC	TGCACGGCTT	TGCCGATCGG	CACGACTACT
701	ACCGCCAAC	TTCTCTGCAA	CCGCTGCTCA	AACAGCTTGC	CAAACCGCTG
751	CTCCTGCTCA	ATGCCGTCAA	CGACCCCTTC	CTCGCGCCCG	AAGCGCTGCC
801	CCCGCGACAG	GAAGTGTCCG	AAGCGGTTAC	CCTGTTCCAG	CGACACACGC
851	GTGGTCATGT	CGGCTTTGTC	GGCAGCACCG	GCGGCAGGCT	GCACCTGCAA
901	TGGTTGCCCG	AGACCGTCCT	GTCCTATTTT	GACAGCTTCC	GCACAAACAG
951	CGGTTAA				

1	MILTPPDTPF	FLRNGNADTI	AAKFLQRSAP	AYRRELLPDS	TGKTKTAYDF
51	SDGISPDAPL	VVLFHGLEGG	SGSHYAVELM	LAUVDRGWNG	VVVFHRSCEG
101	VANTAPVFYH	LGDTAEIAFT	LDTLAARYRE	IYAVGVSLGG	NALAKYLGEQ
151	GENALPQAAA	VISAPVDAAE	AGNRDSGSGIT	RLLYTRYFLR	TLPLKARSLQ
201	GFQTAFAGC	KTLGEFDPR	TAPLHGFADR	HDYYRQTSCK	PLLKHVAKPL
251	LLNAVNDPFL	LPPEALPRAD	EVSEAVTLFQ	PTHGGHVGVF	GSTGGRLHLQ
301	WLPOTVLSYF	DSFRTNRR*			

	10	20	30	40	50	60
a256-1.pep	MILTPPDT	PFFLRNGNADT	IAAKFLQRSAPAYRRELL	PDSTGKTKTAYDFS	SDGISPDAPL	
m256-1	MILTPPDT	PFFLRNGNADT	IAAKFLQRPAPAYRRELL	PDSTGKTKVAYDFS	SDGISPDAPL	
	10	20	30	40	50	60
	70	80	90	100	110	120
a256-1.pep	VVLFHGLEGGSGSHYAVEL	MLAVDRGWNGVVVHFRSCGGV	ANTAPVFYHLGDTAEIAFT			
m256-1	VVLFHGLEGGSSRSHYAVEL	MLAVDRGWHGVVVHFRSCGGI	ANTAPVFYHLGDTAEIAFT			

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGIT					
m256-1	LDTFAARYREIYAVGVSLGGNALAKYLGEQKKALPQAAAVISAPVDAEAAGRRFDSGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLOGFQTAFAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCK					
m256-1	RLLYTRYFLRTLIPKAKSLOGFQTAFAGCKTLGEFDDRFTAPLHGFADRHYYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFGVSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgag ctgcccctgt tcggcgtgga
201 cgacagacag gcggcggatt tggtaataa ggttttggcg gaagtggcgc
251 gtttggaata aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggatt ttttgaact
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIETR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTTCTGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GGCGGGGAC. GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCT CACTGGGTTT CCGTGCGG. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAATA ATTGTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGAAC
351 GKTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNKD EKRNEVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIETR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60

593

```

m257.pep  MGRHFGRQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAD
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRRAADLVNKKVLAELVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAELVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
  1  ATGGGCAGGC  ATTTCTGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
 51  GCGGCGGGGC  GCGGCGGTTT  CTTTCTTGCC  GAATCCTTTT  GCCGCCGATG
101  ATGAAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTTCTGG
151  AAAGGTGTCTG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201  CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTTGGCG  GAAGTGGCGC
251  GTTTGGAAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301  CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGGAACT
351  GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
  1  MGRHFGRRRF  LTVAAVAAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
 51  KGVALGSGAE  LRLFGVDDRR  AADLVNKKVLA  EVARLEKMFS  LYREDSLISR
101  LNRDGYLTSP  PADFLELLSL  AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGRQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNNGDEKRNENVFFWKGVALGSGAX
          |||||          :|||||:|||||:|||||:|||||:|||||:
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      MGRHFGRRRFLTVAAVAAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRRAADLVNKKVLAELVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
||
a257      LRLFGVDDRRRAADLVNKKVLAELVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110

120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgctgta
51  cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtggt gtccgccgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcggtgtt
201 cggttcgcag attgccaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttctcg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggcggcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccga caagaacattt ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtagcga caacgggcgc gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcaaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc ttttttctgg taacctgtct gattgcctcg ctgctgtcga
851 tttttcttgc gctggtaatg gcactgtatt ttgcccgcg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaa gcggtggcgc aggggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcggc cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcca ggaagccgcc cgctactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctacccc ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRFLPIAAI CAVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLK DRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFNDT HEALERSLNL SKSALDLAAD NAVSNAVFPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKGLQT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCTG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TCGTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCGCAG ATTGCCAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCAG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATTG GCGGCAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTTCCTGG CAACCTGCT GATTGCCTCG CTGCTGTCTGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCGG TTTCTGCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA

```


m258 . pep

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

BNSDOCID: <WO 9957280A2 | >

596

	250	260	270	280	290	300
m258 . pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFFLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258 . pep	PVLSLAEGAKAVAQGDQFSQTRPVLNRNDEFGRLLTKLFNHNMTQELSLIAKEADERNRRREEAA					
g258	PILSLAEGAKAVAQGDQFSQTRPVLNRNDEFGRLLTKLFNHNMTQELSLIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258 . pep	RHYLECVLEGLTTGVVVFDEQGLKTFNKAABQILGMPLTPLWGSSRHGWHGVSAQQSLL					
g258	RHYLECVLDGLTTGVVVSYPVLSCCRFAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1027>:

a258 . seq

1	ATGCGCCGTT	TTCTACCGAT	CGCAGCCATA	TGCGCCGTCG	TCCTGTTGTA
51	CGGACTGACG	GCGGCAACCG	GCAGACCAG	TTTCGCTGGCG	GATTATTTCT
101	GGTGGATTGT	TGCGTTCAGC	GCAATGCTGC	TGCTGGTGTT	GTCCGCCGTT
151	TTGGCACGTT	ATGTCATATT	GCTGTTGAAA	GACAGGCGCG	ACGGCGTATT
201	CGGTTTCGCG	ATTGCCAAAC	GCCTTTCCGG	GATGTTTACG	CTGGTTGCCG
251	TACTGCCCGG	CGTGTTCCTG	TTTCGCGGTT	CCGCACAGTT	TATCAACGGC
301	ACGATTAATT	CGTGGTTCGG	CAACGATACC	CACGAGGCGC	TTGAACGCAG
351	CCTCAATTG	AGCAAGTCCG	CATTGAATCT	GGCGGCAGAC	AACGCCCTTG
401	GCAACGCCAT	CCCCGTGCAG	ATAGACCTCA	TCGGCGCGGC	TTCCCTGCCC
451	GGGGATATGG	GCAGGGTGCT	GGAACATTAC	GCCGGCAGCG	GTTTGGCCCA
501	GCTTGCCCTG	TACAATGCCG	CAAGCGGCAA	AATCGAAAAA	AGCATCAACC
551	CGCACAAGCT	CGATCAGCCG	TTTCAGGTA	AGCGCGGTTG	GGAAAAAATC
601	CAACAGGCGG	GTTTCGGTCAG	GGATTGGAA	AGCATAGGCG	GCGTATTGTA
651	CGCGCAGGGC	TGGCTGTCTG	CAGGTACGCA	CAACGGGCGC	GATTACGCCCT
701	TGTTTTTCCG	TCAGCCGGTT	CCCAAAGGCG	TGGCAGAGGA	TGCCGTCTTA
751	ATCGAAAAGG	CAAGGGCGAA	ATATGCTGAG	TTGAGTTACA	GCAAAAAAGG
801	TTTGCAGACC	TTTTTCCTGG	CAACCCTGCT	GATTGCCTCG	CTGCTGTCTGA
851	TTTTTCTTGC	ACTGGTCATG	GCACTGTATT	TCGCCCGCCG	TTTCGTCTGAA
901	CCCGTCCTAT	CGCTTGCCGA	GGGGGCGAAG	GCGGTGGCGC	AAGCGGATTT
951	CAGCCAGACG	CGCCCCGTGT	TGCGCAACGA	CGAGTTCGGA	CGCTTGACCA
1001	AGTTGTTCAA	CCACATGACC	GAGCAGCTTT	CCATCGCCAA	AGAAGCAGAC
1051	GAGCGCAACC	GCCGGCGCGA	GGAAGCCGCC	AGACATTATC	TCAATGCGGT
1101	GTTGGAGGGG	CTGACCACGG	GCGTGGTGTT	GTTTGACGAA	CAAGGCTGTC
1151	TGAAAACCTT	CAACAAAGCG	GCGGAACAGA	TTTTGGGGAT	GCCGCTTACC
1201	CCCCTGTGGG	GCAGCAGCCG	GCACGGTTGG	CACGGCGGTT	CGGCGCAGCA
1251	GTCCCTGCTT	GCCGAAGTGT	TTGCCGCCAT	CGGCGCGGCG	GCAGGTACGG
1301	ACAAACCGGT	CCATGTGAAA	TATGCCGCGC	CGGACGATGC	CAAAATCCTG
1351	CTGGGCAAGG	CAACCGTCCT	GCCCCGAAGC	AACGGCAACG	GCGTGGTAAT
1401	GGTGATTGAC	GACATACCG	TTTTGATACA	CGCGCAAAAA	GAAGCCGCGT
1451	GGGGCGAAGT	GGCAAAACCG	CTGGCACACG	AAATCCGCAA	TCCGCTCACG
1501	CCCATCCAGC	TTTCTGCCGA	ACGGCTGGCG	TGGAAATTGG	GCGGGAGAGT
1551	GGACGAGCAG	GACGCGCAAA	TCCTGACACG	TTCCAGCCGAC	ACCATCATCA
1601	AACAAGTGGC	GGCATTAAAA	GAAATGGTTC	AGGCATTCCG	CAATTACGCG
1651	CGTTCCCTTT	CGCTCAAATT	GGAAAATCAG	GATTTGAACG	CCTTAATCGG
1701	CGATGTGTTG	GCATTGTACG	AAGCTGGTCC	GTGCCGGTTT	GCGGCGGAAC
1751	TTGCCGGCGA	ACCGCTGATG	ATGGCGGCGG	ATACGACCGC	CATGCGGCAG
1801	GTGCTGCACA	ATATTTTCAA	AAATGCCGCC	GAAGCGGCGG	AAGAAGCCGA
1851	TGTGCCCCGA	GTCAGGGTAA	AATCGGAAGC	GGGGCAGGAC	GGACGGATTG
1901	TCCTGACAGT	TTGCGACAAC	GGCAAGGGGT	TCGGCAGGGA	AATGCTGCAC
1951	AATGCCTTCG	AGCCGTATGT	AACGGACAAA	CCGCTGGAA	CGGGATTGGG
2001	ACTGCCCGTG	GTAAAAAAA	TCATTGAAGA	ACACGGCGGC	CGCATCAGCC
2051	TGAGCAATCA	GGATGCGGGC	GCGCGGTGTG	TCAGAATCAT	CTTGCCAAAA
2101	ACGGTAGAAA	CTTATGCGTA	G		

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```

10      20      30      40      50      60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLLK
|||||
a258     MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLLK
10      20      30      40      50      60

70      80      90     100     110     120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
|||||
a258     DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
70      80      90     100     110     120

130     140     150     160     170     180
m258.pep SKSALNLAADNALGNAVFPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
|||||
a258     SKSALNLAADNALGNAIPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
130     140     150     160     170     180

190     200     210     220     230     240
m258.pep SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV
|||||
a258     SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV
190     200     210     220     230     240

250     260     270     280     290     300
m258.pep PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
|||||
a258     PKGVAEDAVLIEKARAKYAE LSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
250     260     270     280     290     300

310     320     330     340     350     360
m258.pep PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
|||||
a258     PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
310     320     330     340     350     360

370     380     390     400     410     420
m258.pep RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL
|||||
a258     RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL
370     380     390     400     410     420

430     440     450     460     470     480
m258.pep AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
|||||
a258     AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
```

598

	430	440	450	460	470	480
m258.pep	490	500	510	520	530	540
	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDQDAQILTRSTDITVKQVAALK					
a258						
	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDQDAQILTRSTDITIKQVAALK					
	490	500	510	520	530	540
m258.pep	550	560	570	580	589	
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258						
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIFKNAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

```

g259.seq
1   atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaactctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgcttcgt tcggtgctgt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaactgctc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccc acgacgaaga cgcgcgacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctc
451 ggcgaaacct atggcgcgct gtctgccgat attttcgagt tgcggcgcc
501 tttggaaagg cgcgcggtta aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

```

g259.pep
1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

```

m259.seq (partial)
1   ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACCC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCC ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACkGACGC GGTCGCCTCG
451 GGCAGAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

```

m259.pep (partial)
1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

151 GETYGRVFAD IFELSALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLOHLEHKPQILALLVKNHGKMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLOHLEHKPQMLALLVKNHGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSALEGRAFKGLMLKT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSALEERRAFKGLILKT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGVGR TQSGVAGDFKNIR					
g259	AEYKXHLRRC LPFGNGVGVGR AQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCGCGATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGC AAAAGG	ATGGCGGAAC	AGGTCAGGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCAATTG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCGCCGAT	ATTTTCGAGT	TGTCGCGCGC
501	TTTGGAAGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHGKG	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTD AVAS
151	GETYGRVFAD	IFELSALEG	RAFKGLMLKT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQAYTEELPPLLSALSAVALVWLAWAFV					

600

	10	20	30	40	50	60
m259.pep	70	80	90	100	110	120
	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
a259	70	80	90	100	110	120
	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
m259.pep	130	140	150	160	170	180
	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVVFADIFELSALEGRAFKGMLKLT					
a259	130	140	150	160	170	180
	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVVFADIFELSAALEGRAFKGMLKLT					
m259.pep	190	200	210			
	AEYKXHLRRLPFGNGVGVGRQSGVAGDFKNIR					
a259	190	200	210			
	AEYKXHLRRLPFGNGVGVGRAQSGVAGDFKNIGKVQ					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGCCTTCGTG TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACCC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PLLSALSASV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCGATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGCCTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATAACCC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGCGGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTCA AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PLLSALSASV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQETIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGK	GMAEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGK	GMAEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRVFADIFEL	SAALE		
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGTT  TTTGACCGC  GCAAATCTGG  TTCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCCGCTC  TGTCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGGTTCTGT  TCGGCGCGTT  CAAAGGCTAA
201 GCGCGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATACACC
251 CCGTCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCAGC  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTTGCATTGG  GGACGGACGC  GGTCGCCTCG
451 GCGGAAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTCGGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAAACTGACG  CGGGAATATA
551 AAAACATCTT  CGGCGATGCC  TGCCGTTCCG  AAACGGCGTT  GGAGTTGGGC
601 GCGCTCAATC  AGGCGTTGCA  GGAGATTTC  AAAACATCGG  AAAAGTCCAA
651 ACGGATATTT  TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALLVKNHGKG  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDAS
151 GETYGRVFAD  IFELSAALEG  RAFKGMLKLT  AEYKNIFGDA  CRSETALELG
201 ALNQALQEIS  KTSEKSRIF  Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGK	GMAEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGK	GMAEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	AVASGETYGRVFADIFEL	SAALEGRAFKGMLKLT		
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELG	ALNQALQEISKTSEKSRIFYX				
m259-1	AEYKNIFGDACRSETALELG	ALNQALQEISKTSEKSRIFYX				
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

g260.pep

m260.seq

m260 . pep

m260/g260

BNSDOCID: <WO__9957280A2 | >

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

```
a260.seq
1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGGCGC GGCAGCGGTT TCTTGCGGG AAACGATTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GCGCGAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTGTCC
551 CGAAATGCCC CACAGGTGT CGCCCTGTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

```
a260.pep
1  MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVQV AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*
```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG DVFIDSVQV					
a260	MGAGMVFVVF RPFSSLFRL FEDRVGIVEG AHDAAECDL PEEFTRIRIG DVFIDSVQV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL RMPHKDAVEV DIDGGNTVSG					
a260	AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL RVPHKDAVEV DIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH QYLVRINQVG IVDLIPVRVPQ					
a260	HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH QYLQINQVG IVDLIPVRVP QAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

```
g261.seq
1  atggagcttg ggcataatcgt attccttgctg ctttgcgcgcg gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctcgggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctggttcgcg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtag atcagcgcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcatt gatttgacga acacgccgcg
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcgggc gtttcgatgg cggcggtttc gtccatcagg gcgttgtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcccgcgga tccactctgc gcgttcagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttgattg
```

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag
701 gctttttggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
51 LFADVVQHAH FVRQRPRLRL GQVHQRVDL KIVVHRQIKG NVHGFDEHAA
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
201 VSEGDGLDVF APVGLDCLNQ AGGRILTARE DDQGLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCCACG
201 TTTGCGCCTT GGTCAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTTGACAA ACACGTCGCG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GgCTcAAGTC GAGTACGGT TGTTCGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51 LLADIVQHAH FVRQRPRLRL GQIHQRVDL KIIVHRQIKG NVHRFDKHVA
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAPVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

m261.pep	10	20	30	40	50	60
	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVVQHAH					
	10	20	30	40	50	60
m261.pep	70	80	90	100	110	120
	FVRQRPRLRLGQIHQRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
g261	FVRQRPRLRLGQVHQRVDLKIIVHRQIKGNVHGFDEHAA AVGIARKIGFAHARDDVPDT					
	70	80	90	100	110	120
m261.pep	130	140	150	160	170	
	LPFGVNRGIEQEKRVAAVYKIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVQVEYGLF					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130	140	150	160	170	180
m261.pep	180	190	200	210	220	230
	DAQILRNPAFTFQLDGMALPVLESNGLDVFAPVGLDCLNQAGGRILTARKDDQGLLVX					
g261	DTQILRDPLCAFQLDGMALPVSEGDGLDVFAPVGLDCLNQAGGRILTAREDDQGLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAG
201 TTTGCGCCTT GGTGAGATAC ATCAGCGGCG TGTGGATTTC AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTT CCGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGCGATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTGACGCG CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHGFDPKHT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHAHARDDVPYP					
a261	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHGFDPKHVTAAGIAGEVGFHAHARDDVPYP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI VRNLPHQAV EYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGI VRNLPHQAV EYGLFDAQIL					
	130	140	150	160	170	180
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI LTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI LTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgcca
51  accgcgcta gaggccgtac caaaaaaca cggctttatc cccaacctca
101 tcggcgatt ggcaaacgcc cccgaagctt tggcgttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcgaag tcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acacaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccg ctttgccggc aggtaaatct gacgatgcc aactcggcgc
351 gcttgccgc ttcacccaag ccgtaatggc gaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

g263.pcp

m263.seq (partial)

m263.pep (partial)

m263/g263

a263.seq

a263.pep

BNSDOCID: <WO__9957280A2_| >

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

BNSDOCID: <WO 8957280A2 | >

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

```

      10      20      30      40      50      60
m264 . pep  LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ
      |||||
g264        LTLTRKTLFLLTAAFGTHSLQTASADAVV KPEKLHASANRSYKVA-----EFTQ
      10      20      30      40

      70      80      90     100     110     120
m264 . pep  TGNASWYGGRFHFGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP
      |||||
g264        TGNASWYGGRFHFGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP
      50      60      70      80      90     100

      130     140     150     160     170     180
m264 . pep  FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ
      |||||
g264        FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFSGTEHEAQ
      110     120     130     140     150     160

      190     200     210     220     230     240
m264 . pep  AYLNQAAQNFAVSSSGTNLSVEKRRY EYVVKMGPFTSQERAAEAEQA RGMVRAVLTAGX
      |||||
g264        AYLNQAAQNFAASSSSPNLSVEKRRY EYVVKMGPFA SQERAAEAEQA RGMVRAVLTSGX
      170     180     190     200     210     220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTC CTCACCGCCG CATTCCGGCAT
51  ACATTCCTTT CAGACGGCAT CCGCCGACGC AGTGGTCAGG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAA ACGCTACACG
151 CCGAAAAAAC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAATT GGGCTTTGTC AACCAAGGGA CGGCGCACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACC GTT GCCGAAAACA AAGACATCTT
501 CATCGACTTG AAATCTTTTCG GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAACCTG GCTTCATCGG CATCAAACCC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTGCCTC
651 GCAGGAACGC GCCGCCGAGG CCGAAGCTCA GGCGCGCGGT ATGGTTCCGG
701 CGGTATTAAAC CGCCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

```

1   LTLTRKTLFL LTAAFGIHSF QTASADAVVR AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGR FHGRKTS GGE RYDMNAFTA HKTLPIPSYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAQKLG FV NQGT AHVKIE
151 QIVPGQSAPV AENKDIFIDL KSFGTEHEAQ AYLNQAAQNL ASSASNP NLS
201 VEKRRY EYVV KMGPFA SQER AA EAEQA RGMVRAVL TAG*

```

m264/a264 96.2% identity in 239 aa overlap

```

      10      20      30      40      50      60
m264 . pep  LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ
      |||||
a264        LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ
      10      20      30      40      50      60

```

609

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGT NLSVEKRRYEVVVKMGPF TSQERAAEAE AQARGMVR AVLTAGX					
a264	AYLNQAAQNFAVSSSGT NLSVEKRRYEVVVKMGPF TSQERAAEAE AQARGMVR AVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTGGCTTG
51  GCGCGCGCTG ATGATTTTGT CTGTGTTGTT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGCGGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT .TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTCGGCTTC GCGCGCGCGT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
1  MSVILPPTRA NAAFAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLENV DINKVSNNRQ PAVNTARTI PRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTI PRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

a265.seq

```

1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGCGCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... ..GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTCC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

a265.pep

```

1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*

```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANAFAFAWRLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
a265	MSVILPPTRANAFAFAWRLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFIKFAFVNRGLNVNDINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
a265	KRRRLKFI---FAPAKYLXXCLKDVKAGHQP VNTARTIPRAXASASAARSCEANGPILT					
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

g266.seq

```

1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccacatcatg
51  accgcatcca tgtacatcct tttggtcttg gcaactcatct ttgccaacgc
101 ccccttcctc acgaccagac tggttcggtc ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg cagggttcgc gctgaccgcc
201 tctcttgccct acatcctcga atcccggtgc ggagcggtac acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgtttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa

```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

g266.pep

```

1   MQFRRHRRRO CPNRKPIMTA SMYILLVLAL IFANAPFLT RTFGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGW EFWA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

m266.seq

```

1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CCGTACACGA TCAGGGTTGG GAGTTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTTG CGTTTCCATG TTTTGTGTGG CCGTATTTTT GGCACACGCG
351 CAACAGGGAA TAG

```


This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          60      70      80      90     100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCTT
101  TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CCGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC CGTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTLKLFIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90     100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq

This corresponds to the amino acid sequence <SEQ ID 1076; ORF 267.ng>:

g267.pep

1 MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGOVDVV TLGAAGAVFA
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLFGKI
101 NCVFAGKKVF ERYAHAFDOF AKOKGFY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1077>:

m267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACCG	GATACACCGC	TCTTCGCCGT	TCGGATACCG	CcGTGCGCG
251	TGCAGACCGC	GGAAACGCAC	GGATTGCGGC	GTTTTCTCTT	CGGGGAAATA
301	AATTGTGTCT	TTCGGGCGCA	AAAAGTTTTT	GACCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAAGTTTTTA	GAA	

This corresponds to the amino acid sequence <SEQ ID 1078; ORF 267>:

m267.pep

1 VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGOVDVV TLGAARTVFT
51 FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI
101 NCVFAGEKVF ERYAHTFYQF AKOKGFY*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 267 shows 82.7% identity over a 127 aa overlap with a predicted ORF (ORF 267.ng) from *N. gonorrhoeae*:

m267/g267

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1079>:

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCTTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TCGCCATTGC	GGGGCAAACG	GCTTCACACA
201	ATTTACACGC	GATGCACGCT	TCCTCGCCGT	TTGGATAACG	GCCTTGC GCG
251	TGCAGACCGC	GGAAACGCAT	AGATTGCGCG	GTTTTCTCTT	CGGGAAAATA
301	AATCGTGTCT	TGCGCGGCAA	GGAGCTTTTT	GACCGCTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAGG	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
m267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPFAVRI	PPLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGKIN	RVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaatctt
101 cctgcggaag cgaagagact aaagagatct tgggtcaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcacga
351 tgttgatgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgac gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctgggtgtc tatggcactg attaaagagc cggttgacaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651 ggcagaagaa gcggcggcgc aggaggcatt gggctgggag caggaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccacaatat
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVDR
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAAL KLDVDDVVD YAVAANQSIG NSHKTPDFF EPYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAREAE AAAQEALGRE QEAAVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASOK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCh TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   .MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL POTVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADKKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

m268.pep                               10      20
                                     MALIKEPLDKVKQRNEELEAAE-----
g268                                |||||:|||||:|||||
SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
160      170      180      190      200      210

m268.pep                               30      40      50      60      70      80
--EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTVQNKLP SQKTWKSMD
g268                                |||||:|||||:|||||:|||||:|||||
AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQNKLP SQKTWKSMD
220      230      240      250      260      270

m268.pep                               90      100     110     120     130     140
KICANNAKAEKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADKKELSKRLX
g268                                |||||:|||||:|||||:|||||:|||||
KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

a268.seq

```

1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

a268.pep

```

1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL POTVQNKLP SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

m268.pep                               10      20      30      40      50      60
MALIKEPLDKVKQRNEELEAAEEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
a268                                |||||:|||||:|||||:|||||:|||||
MALIKEPLDKAKQRNEELEAAEEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

615

	10	20	30	40	50	60
m268.pep	70	80	90	100	110	120
	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
a268	PQTVQNKLPQSQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	70	80	90	100	110	120
m268.pep	130	140				
	KALIDEMXREADXKELSKRLX					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.pep

```

1  VQSRDGLHKKFKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

m268-1.pep		10	20	30	
		VQSRDGLHKKFKHICSAAMALIKEPLDKVKQRNE			
g268	150	160	170	180	190 200
	KEGAYVYKTISYSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE				
m268-1.pep	40	50	60	70	80
	ELEAAE-----EAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
g268	210	220	230	240	250 260
	KLEAAEATAQEAREAEAEAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN				
m268-1.pep	90	100	110	120	130 140
	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE				
g268	270	280	290	300	310 320
	KLQASQKTWKSMDKICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRKKALIDE				
m268-1.pep	150	159			
	MAREADKKELSKRLX				
g268	MVREEDKKELPKRLX				
	330				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

401 TGCACAACCG TAAAAAGCC CTTCTGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LDEMAREAD
151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKQRNEELEAAE	EAQALGREQEVDRVSEW				
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVQRNEELEAAE	EAQALGREQEAARVSEW				
	10	20	30	40	50	60
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGETP	NGIKFSEL			
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGKTP	NGIKFSEL			
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGETP	NGIKFSEL			
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKS	GMKICANNAKAEGKTP	NGIKFSEL			
	70	80	90	100	110	120
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggaacg gcggcgctga ttttttcgct
51 cagcccttgg atttgggcgg tgggtggtg gtggtcgcg tcggtttttt
101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttggcg
151 gtttcgccgt gggactttat ccggaacacg gcttcgcccc aggtgtcggc
201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc
251 cgcccggttc cattttgctg tccaatcgcg ggggttaaaaa accgttgctg
301 tttaagtcgc cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc
351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTTGT
101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCTGTC GTTGATGGTT
151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC
201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TTAAAAAGCC GTTGTCTGTT
301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IAAVWWSR SALSCKPCAT CPRPAPALMV
51 SPWDFIQTNT SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269      MVWRVNCAATAALIFSSSPWIWAVVWWSRSASFCKPCASLDASSAPALAVSPWDFIRNT  60

m269.pep  ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS  119
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269      ASPKVSAAALMHSEKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDTALLCLSLRS  120

m269.pep  SX  121
          ||
g269      SX  122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCGCGT CCAGCGCGCC GGC GTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTTA AAACCCAGGC TTTGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTGC
301 TTTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAAAL HSEKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269.pep  10 20 30 40 50 59
          MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
a269      10 20 30 40 50 60
          MVWRVNCAATAVLIFSSSPWIWAAVWVWARSALSWRFCASVPASSAPALTVPWDFIQNT

m269.pep  60 70 80 90 100 110 119
          ASPKVSAAALMHSEKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDTALLCLSLRS
a269      60 70 80 90 100 110 120
          ASPKVSAAALMHSEKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDTALLCLSLWS

m269.pep  120
          SX
          ||
a269      SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcactgctgc tgactgcctt
51 tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccc cggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg gggttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcac cgcctgcccc tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

g270.pep

```

1  MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca. CAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCCTTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKL LLA AALLLIAFAAVKLVLLQWWQAXQPQAVAAQC					
g270	MNKNRKL LLA AALLLTAF AAF KLVLLQWWQAQQPQAVAAQC					
	10	20	30	40	50	60
	70					
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARIRLPICVEGRR					
	70	80	90	100	110	120
	70					
	130					
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq

```

1  ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
51  TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
101 AAGCTGTGGC GCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT
401 AGACGGCATT TACCGCCGAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep

```

1  MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
51  GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

```


101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
a270	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPF	DIYIE	HAPAG	TEQVS	ISFS	MKNMD
a270	TKKPF	DIYIE	HAPAG	TEQVS	ISFS	MKNMD
	70	80	90	100	110	120
	130	140				
m270.pep	DFTAD	ITIGS	RTFQT	AFTAE		
a270	DFTAD	ITIGS	RTFQT	AFTAE		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcggatggc	gaggatttgg	gcgacggggg	taacgttgtg
51	tatggtcagt	ccgtgtccgg	cgttgacgac	caagcccaaa	tcgccggcga
101	aatgcgcgcc	gttttgatg	cgctcgaact	gcctgatttg	ttcggcggtg
151	ctttgtgctg	cgccatagtc	gccggtgtgc	agctcgacaa	cgggcgcgcc
201	gacatcacgg	gcggttggga	tttgctgtgc	gtcggcatcg	ataaacaagg
251	acacgcgtat	gcccgcgtcg	gtcaggattt	tggcgaattc	ggcgattttt
301	tcctgttgcg	ccaatacgtc	caaaccgcct	tcggtcgtga	tttcctgccg
351	tttttcaggc	acgatgcaca	cgtcttccgg	catcacttta	agcgcgtttt
401	cgagcatttc	ttccgtcaac	gccatttcaa	ggttcaggcg	cgtgcggatg
451	gcgtttttga	cggtcaatac	atccgcgtct	ttgatgtggc	ggcggtcttc
501	gcgcaggtgc	atggtaatac	ggtctgcacc	gtgcgtttcg	gcaaccagtg
551	ccgcctccac	ggggctggga	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTL	CMVS	PCPAL	TTKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LCASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTR	MPAS	VRILANS	AI
101	SCCANTSKPP	SVVISCR	FSG	TMHTSS	GITL	SAFSSIS	SVN	AISRFR	RVRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIRSA	PCVS	ATSAAST	GLG	*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTcagTT	CGCGGATGGC	GAGGATTtGG	GCGATGGGGG	TAACGTTtGTG
51	TATGGTcAGT	CCGTGTCCGG	CGTTGACGAC	CAAGCCCAAA	TCGCCGgCGA
101	AATGCGCGCC	GTTTTGGATG	CGCTCGAACT	GCCTGATTtG	TTCCGCGTgG
151	CTGCGCGCGT	CGGCATACGC	GCCTGTGTGC	AGCTCGACAA	CGGGCGCGCC
201	GACATCACGG	GCGGCTTGGa	TTTGCCTGTC	GTCCGCATCG	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTCG	GTcAGGATTt	TGGTGAACCC	GGCGATTtTT
301	TCCTGTtGCG	CCAATACGTC	CAAACCGCCT	TCGGTcGTGA	TTTCCTGACG
351	TTTTTCAGGC	ACGATGCACA	CGTCTTCCGG	CATCACTtTC	AAAGCGTtTT
401	CCAACATTTC	TTCCGTCAAC	GCCATTtCAA	GGTTCAGGCG	CGTGCgGATG
451	GCGTtTTTGA	CGGCAACAC	GTCCGCGTCT	TTGATGTGGC	GGCGGTCTTC
501	GCGCAGGTGC	ATGGTAATCA	AATCCGCACC	GTGCGTtTCG	GCAACCAGTG
551	CCGCCTCCAC	GGGGCTGGGA	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTL	CMVS	PCPAL	TTKPK	SPAKCAP	FWM	RSNCLIC	SAW
51	LRASAYAPVC	SSTTGAPT	SR	AAWICL	SSAS	INKDTR	MPAS	VRILVNP	AI
101	SCCANTSKPP	SVVISXRF	SG	TMHTSS	GITF	KAFSNI	SVN	AISRFR	RVRM
151	AFLTANTSAS	LMWRRSS	RRC	MVIKSA	PCVS	ATSAAST	GLG	*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

```

      10      20      30      40      50      60
m271 .pep  XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRLASAYAPVC
      |||||
g271       MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC
      10      20      30      40      50      60

      70      80      90     100     110     120
m271 .pep  SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG
      |||||
g271       SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANS AIFSCCANTSKPPSVVISCRFSG
      70      80      90     100     110     120

      130     140     150     160     170     180
m271 .pep  TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVKSAPCVS
      |||||
g271       TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRCMVIRSAPCVS
      130     140     150     160     170     180

      190
m271 .pep  ATSAASTGLGX
      |||||
g271       ATSAASTGLGX
      190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271 .seq

```

1  ATGTTTCAGTT CGCGGATGGC GAGGATTTGG GCGATGGGGG TAACGTTGTG
51 TATGGTCAGT CCGTGTCCGG CGTTGACGAC CAAGCCCAAA TCGCTGGCAA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTGGA TTTGCCTGTC GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT GCCCGCGTCG GTCAGGATTT TGGTGAATTC GGCAATTTTG
301 TCTTGTGTCG CCAATACGTC CAAGCCGCCT TCGGTGCTGA TTTCTTGACG
351 TTTTTCGGGC ACGATGCACA CGTCTTCGG CATCACTTTA AGCGCGTTTT
401 CGAGCATTTC TTCCGTCAAC GCCATTTCAA GGTTCAAGCG CGTGC GGATG
451 GCGTTTTTGA CAGCAAACAC GTCCGCGTCT TTGATGTGGC GGCGGTCTTC
501 GCGCAGGTGC ATGGTAATCA GGTCCGCACC GTGCGTTTCG GCAACCAAGT
551 CCGCCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271 .pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTSKPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

```

      10      20      30      40      50      60
m271 .pep  XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRLASAYAPVC
      |||||
a271       MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC
      10      20      30      40      50      60

      70      80      90     100     110     120
m271 .pep  SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG
      |||||
a271       SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNNAISRFRRVRMAFLTANTSASLMWRRSSRRRCMVIKSAPCVS					
a271	:: :					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271						
	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcgatgg ctgcgccata tgaacaaaaa
51  caaagggtcc gacctgtttg tgacgacca tttcccgccc gctatgaagc
101 tggacggcaa aatcaccgcg atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcatcgacc aacgagtgcg atttcgccat cagcctgccg gacaccagcc
251 gcttccgcgt caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttgcgc tgaaaaaacg cgggctgggt atttttgcg
401 gcggcaccgg ctcgggcaaa tcgacttcgc tcgcctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcgttga aaaatacgct gcgtcaggcg
601 ccgatgtgta tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc tttgccgaaa cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctcgaccgca tcatcaactt cttcccgag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgctcgttc cgcgagacgg cggcaagggc aggggtggcg
851 cagtgcaggt gctgctcaat tcgcccctga tttcggagtt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgcgt
1051 ttggcggtac agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPPALK DVALKKRGLV IFVGGTGSBK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETM DYAI FAETGHL CMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMO TFDQHL YQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTCC TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCAGGACG AACCGCTGAC GCGCGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 CGGCAACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG

```

```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTCCCCGAG
751 GAGCGGCGCG AACAAATGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCcGA TTTCGGAGTT GATTCACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAAATGCCG ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCCGATT
1101 GGnACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272 . pep

```

1  MTAKEELFAW LRHMxQNKGS DLFVTTTFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IORGATALVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTGSCK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIA FAETGHLCA TLHANSTNQA LDRIINFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMOF FDQHLQLYE KDISLQAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272 . pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGS DLFVTTTFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKGS DLFVTTTFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272 . pep	70	80	90	100	110	120
	AKQAEFSSTNECNFAISLPDTSRFRVNAI IORGATALVFRTITSKIPKFS ESNLPPVVK					
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAI IORGATALVFRAITSKIPKFS ESNLPPALK					
	70	80	90	100	110	120
m272 . pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTGSCKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTGSCKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
m272 . pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCA TLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCA TLHANSTNQA					
	190	200	210	220	230	240
m272 . pep	250	260	270	280	290	300
	LDRIINFPEERREQLTDL SLNLQAFISQRLVPRDGGKGRVAAVEVLLN SPLISELIHN					
g272	LDRIINFPEERREQLTDL SLNLQAFISQRLVPRDGGKGRVAAVEVLLN SPLISELIHN					
	250	260	270	280	290	300
m272 . pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMOF FDQHLQLYE KDISLQALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMOF FDQHLQLYE KGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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```

          370
m272 . pep    QSXSPDLXLLX
              || :||| |||
g272         QSSDPDLELLX
              370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272 . seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCG TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGTCG
401 GCGGCACCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTTCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AACTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTCCG GTCCCGATT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272 . pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRV NAM IQRGATALVF
101 RAITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVD TENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHL CMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLYQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272 . pep    MTAKEELFAWLRHMKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
              ||||| :||| ||| ||||| ||||| ||||| ||||| ||||| |||||
a272         MTAKEELFAWLRHMKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
              10      20      30      40      50      60

          70      80      90      100     110     120
m272 . pep    AKQAEFSSTNECNFAISLPDTSRFRV NAMIQRGATALVFRTITSKIPKFESLNLPVLK
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a272         AKQAEFSSTNECNFAISLPDTSRFRV NAMIQRGATALVFRAITSKIPKFESLNLPVLK
              70      80      90      100     110     120

          130     140     150     160     170     180
m272 . pep    DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a272         DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
              130     140     150     160     170     180

```

	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272.pep	LDRIINFPEERREQLLTDSLNLQAFISORLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFPEERREQLLTDSLNLQAFISORLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272.pep	GNIHEIKEVMKKSTTLGMOTFDQHLYQLYEKGDISLOEALKNADSAHDLRLAVQLRSRRA					
a272	GNIHEIKEVMKKSTTLGMOTFDQHLYQLYEKGEISLQDALKNADSAHDLRLAVQLRSRQA					
	310	320	330	340	350	360
	370					
m272.pep	Q SX S P D L X L L X					
	:					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273.seq

```

1  atgagtccttc aggcgggtatt tatatacccc ccaagccgta cgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcaccg ttttcctgcc gtttcctgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcggggcg gtgcccgtga aatcaaggcg
351 gtttgagaag tgtttcenac gcgcccgcgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccctg ctttttggtt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVFQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273.seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTTCATT
251 GTTGTTCCTT AATGCTTAAA AACC CGCTG TCCGTGCAAC CGTTTTAAGG
301 CGGCAAATTG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTTGtKtWTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273.pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLL V AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQSKHADRCQDIGVFKAGTPFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQSKHTRRQDIGVFEAGTFPTVFLPLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRA-ALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

1	ATGAGTCTTC	AGGCGGTATT	TGTATACCCC	CCAAGCCGTA	CCGCACAATA
51	CAACGAAAT	CAGGAAAACG	GCGGTAAAGC	TCATAAACAG	GGACAAAGCG
101	GCAAACACGC	CGACCGCCGT	CAGGATATAG	GCGTATTCCA	GACCGGAACT
151	CCATTACCG	TTTTCTGCG	GCTTTTGTG	GCTTTTGAA	TAAAGGATGA
201	TGCCGGCAAG	CAGCGCGGCA	GCCGCGCCCG	ACATTAGCAT	AATGTTCATT
251	GTTGTTCTT	AACGGTTAAA	AACCCGCCCC	TCCGTGCAAC	CGTTTTTAAG
301	AGGCGGTAA	TCACAAAGTT	TGTTGGCGGA	CGTGCTCTCT	TACAATCAGG
351	GCGGTTTAA	GGGCATGATG	CACTGCCCCG	TGTGCCGGAT	ATTATTTGTC
401	GCTCACCTGC	AAAATTGCCA	AGAACGCGCT	TTGCGGGATT	TCCACATTGC
451	CCACTTGTTT	CATACGGCGT	TTGCCTGCTT	TTTGTTTTTC	AAGCAGTTTT
501	TTCTTACGCG	TAA			

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

1	MSLQAVFVYP	PSRTAQYNEN	QENGGAHKQ	QSGKHADRR	QDIGVFQGT
51	PFTVFLPLFV	AFEIKDDAGK	QGRSRARH*	NVHCCSLTVK	NPPVRATVFK
101	RR*ITKFVGG	RALLQSGRFK	GHDALPRVPD	IICRSPAKLP	RTRFAGFPHC
151	PLVSYGVCLL	FVFQAVFSYA	*		

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQSKHADRCQDIGVFKAGTPFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGSQSKHADRRQDIGVFQGTPTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRAALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
a273	GHDALPRV-PDIICRSPAKLPTRFAGFPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC  CGATTTTGT  CGTCatCGCC  AgcgTCGCTA  TGTTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAGGATG
101 GCAAGCATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTCCT  CATTCTCCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTCGGC  ggCgagtTTG  ACGGCAAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTgt  tcaaAACCCCT
351 TCCGCCGGCC  AACCCTGGT  ATGTGCGCGT  GGAggacgCG  GCAGGCGTGT
401 GGCAGCGTCGA  GAACAAATGG  ATTACCAGCC  AGGCAATGC  GGTCGATTTG
451 ACCCCGATGG  ACAACTTTT  CAATAATGCA  GGAAGCAAAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTLPPA  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNA  GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC  CGATTTTGT  CGTCATCGCC  AGCGTCGCTA  TGTTTTTTGT
51  CGCGCAGCAG  CACGCGACAG  ATTTGGTTAC  GGACGATTAT  TATAAAGACG
101 GCAAACATAT  CGACATCCAG  CTTTCATCGG  ATGAAGAAGC  CGTCAGACGG
151 CATATCGGGG  TGCAGGTTCT  CATTCTCCCC  GATATGAATG  CGGCAAAAGT
201 GTTTGTCGGC  GCGGAGTTTG  ACGGCAAACA  GCCTTTGAAC  CTGCTGCTGA
251 TGCACCCGAC  CCGCAAGGCG  GACGATCAAA  CCGTCGCCCT  CAAGCCCGTC
301 GGCAGCGCGC  AGAACGGCAG  GCGGAATAT  GAGGCGGTGT  TCAAACCCCT
351 TTCGCCGACC  AACCCTGGT  ATGTGCGCGT  GGAGGACGCG  GCAGGCGTGT
401 GGCAGCGTCGA  GAACAAATGG  ATTACCAGCC  AAGGCAATGC  GGTCGATTTG
451 ACCCCGATGG  ACAAGCTTTT  CAATAATACT  GAAAGCAAAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA  SVAMFFVAQQ  HATDLVTDDY  YKDGHIDIQ  LHRDEEAVRR
51  HIGVQVLISP  DMNAAKVFG  GEFDGKQPLN  LLLMHPTRKA  DDQTVALKPV
101 GSAQNGRAEY  EAVFKTSLPT  NHWYVRVEDA  AGVWRVENKW  ITSQNAVDL
151 TPMDKLFNNT  ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
g274.pep	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTSLPT					
	70	80	90	100	110	120
g274.pep	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTSLPT					
	70	80	90	100	110	120
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGT TTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCC GATATGAATG CGGCAAAAGT
201 GTTTGTCTGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGC GCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451 ACCCGATGG ACAAACTTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTSLPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
a274	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
a274	DMNAAKVFGV GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTSLPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQNAVDLT PMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggcgacga tgatgccggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cggtcggatt cggtgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaaatgg cgcgggcatg
201 ggcgacgcgt tgccgctgtc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgcgagc ggggatgcgt cgatcaggct ttgcagggtg
301 gcggcttgga gggcggacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggacg ttttcaaca ggggtgtcgtc aaacaggaat acgtcttggg
401 agacgagggc gaattggcgc gcaggcagc cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaagggtg acgacggtgg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgtctg atgtcgaggt tgaagttgtc gagggctttg
601 atgccgtctg aacggtattc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgca gcgtgccttt gtccgtgttc ggcgggggtg
701 cgagaaatgc acatacgccg tcggcggcga ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

```
g276.pep
```

```

1  MILPPSMTMM RSADSTVVRR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGRRRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

m276.seq

```

1  ATGATTTTGC CGTCGTCAT CACGATGATG CGGTCGGCCC CTTGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATCGA CGCGGGCAAT
201 GGCGACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGGA GGGCGAACAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTCTGC AAACAGGAAT ACCTCTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGCGGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTG ACGACGGTGG ATTTGCCGCT GCGGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGCGTGCGA GCGTGCCCTT GTCCTGTTCG GGCGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGGG GCGTACATTT GCAGCATCGC
801 GACGATGAAT GCCATAAAT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

m276.pep

```

1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGSRLL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
g276	MILPSSITMMRSADSTVVRRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSRLLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKRGSRLLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

a276.seq

1	ATGATTTTGC	CGTCGTCCAT	TACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGGCGG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTCC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCCAA	TGCGCTGGTG
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGTCT	TTCAAATGG	CGCGGGCAAT
201	GGCAACGCGT	TGCCGCTGTC	CGCCGGATAA	GTTGCTGCCG	TTCGATCCGA
251	TGGGCTGGTG	CAGTCCGAGC	GGTGATGCGT	CGATCAGGCT	TTGCAGGTTA
301	GCGGCTTGGA	GGGCGGATAG	GACTTCGGCT	TCGCCC GCGT	CGGGACGGCT
351	ATATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTTGGG
401	AGACGAGGGC	AAATTGGGCG	CGCAGGCAGT	CGAGTTTGAT	GTCGGCGATG
451	TCGATACCGT	CTATGCAGAT	GTTGCCGGCA	GACGGTTCGA	CAAAGCGGGG
501	CAGCAGGTTG	ACGACGGTGG	ATTGCGCGCT	GCCGGAACGT	CCGACCAAGG
551	CGACGCGTTC	GCCTTGCTGT	ATGTCGAGGT	TGAAGCCGTC	GAGGGCTTTG
601	ATGCCGTCCG	AACGGTATTC	GACATCGACG	TTGCGGAAGC	TGATGCGCCC
651	TTGACACGCG	TGCGGTGCGA	GCGTGCCTTT	GTCCTGTTCT	GGCGGGGTGT
701	CGAGAAATGC	ACATACGCCG	TCGGCGGCGA	GGAACATCGT	CTGCATAGGG
751	ATGCTAATGT	TGGCAAGGCT	TTTGATGGGG	GCGTACATTT	GCAGCATCGC
801	GACGATGAAT	GCCATAAATT	CGCCGATGGT	GGTGTAG	

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

a276.pep

1	MILPSSITMM	RSAPSMVVR	WATMMPVRF	IRRSSACWTR	RSDSLSNALV
51	ASSNNNIGAS	FKMARAMATR	CRCPPDKLLP	FDPMGWCSPS	GDASIRLCRL
101	AAWRADRTSA	SPASGRLYRT	FSNRVSSNRN	TSWETRANWA	RRQSSILMSAM
151	SIPSMQMLPA	DGSTKGRSRL	TTVDLPLPER	PTRATRSPCL	MSRLKPSRAL
201	MPSEYSTST	LRKLMPSTR	CGASVPLSCS	GGVSRNAHTP	SAARNIVCIG
251	MLMLARLLMG	AYICSIATMN	AINSPMVV*		

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRF					
a276	MILPSSITMMRSAPSMVVRWATMMPVRF					
	10	20	30	40	50	60
m276.pep	70	80	90	100	110	120
	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGEL					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGEL					
	70	80	90	100	110	120
m276.pep	130	140	150	160	170	180
	FSNRVSSNRNTSWETRANWARRQSSILMSAMS					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMS					
	130	140	150	160	170	180
m276.pep	190	200	210	220	230	240
	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKL					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKL					
	190	200	210	220	230	240
m276.pep	250	260	270	279		
	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtacat cgccaagcgt
101  tcgatgccgt aggtaatctt gccgagtagc ggcgtgcaat cgataccgcc
151  gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201  cttcccagcc caaacccac gcaccgaggg tgggggtttc ccagtcgtct
251  tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgcag
301  ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgaggcgca
351  cttggaattg gtaatagtgt tgcaggcggg tgggggtgtc gccgtagcgg
401  ccgtcttttg ggcggcggct gggttggacg taggcggcaa accaaggctc
451  gggggccgagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501  cttccatgtc gaagggttg atgacgggtc agcctttgtc tgcccagaag
551  gtttgcagtt tgaagatgat ttggtggaag gtaagcatgg cttattgttc
601  gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651  tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH ROAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG Y FHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101  GVEIEVLDI G GGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPR L
151  GAERAQAGG MGCAGTDFHV EGLDDGAAFV CPEGLQFEDD LLEGKHGLLF
201  DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAC TGG
101  CGCAGCAGCC AGTCGGCATC GCTGTATTTC AAGTTGTAGG TGGATTGCTC
151  GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTGCA
201  GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251  ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301  GTCGATGCCG CCGACTTGTT GGAAATAGGT AACTGGGTT ACTTCCATGC
351  CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401  TCCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451  CAATTGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501  GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551  TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601  AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651  TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701  TCTGCCAGA ATGTTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751  GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG AVFEVVGGLL
51  DFVLVVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101  VDAADLLEIG KLG Y FHAVEP DFPAQTPRAE GGVFPVVDK ADVVDGIDA
151  QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201  KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251  GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

```
g277.pep
10 20 30
MVHVAVAYGIAVRRFCPNEVIDVFHALQVH
```

631

```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVGDGVAVERFCPNEVVDVFYTLQVH
           30      40      50      60      70      80
g277.pep  RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHVEPDFFPAQTPRTEGGVFPVVFDDKADVV
           40      50      60      70      80      90
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHVEPDFFPAQTPRAEGGVFPVVFDDKADVV
           90     100     110     120     130     140
g277.pep  DFGIDAQFAQGVIEVLDIGGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           100     110     120     130     140     150
m277      DFGIDAQFAQGVIEVLDIGGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           150     160     170     180     190     200
g277.pep  GAERAQAGGGMGCAGTDFHVEGLDDGAAAFVCPEGLQFEDDLLEGKHGLL
           160     170     180     190     200
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51 TTTCTTCGCG AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAC TGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCT AGATTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTCGACAAA GCGGATGTCG TGCAC TTTGG GGTTCGATGCC
451 CAATTCGCGC AGGGAGTCTGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCGAGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGCGGCGCG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDD ADVVHFGVDA
151 QFAQGVIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

m277.pep  10      20      30      40      50      60
MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAV
|||||
a277      10      20      30      40      50      60
MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLDFVLVVHVAV
|||||

m277.pep  70      80      90      100     110     120
GDGVAVERFCPNEVVDVFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHVEP
: : : : :
a277      70      80      90      100     110     120
SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
|||||

          130     140     150     160     170     180

```

```

m277.pep    DFPAQTPRAEGGVFPVVFDDKADVVDFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQA
a277        DFPAQTPRAEGGVFPVVFDDKADVVHFGVDAQFAQGVIEVLDIGGSGLEGDLELVIVLQA
              130      140      150      160      170      180

              190      200      210      220      230      240
m277.pep    VGVVAVAAVFGAAAGLDVGGKPRLGAECAQAGGMGCAGTDFHVEGLDDGAAAFVCP ECLQ
a277        VGVVAVATVFGAAAGLDVGGKPRLGAECAQTGGGMGCAGTDFHVEGLDDGAAAFVCP ECLQ
              190      200      210      220      230      240

              250
m277.pep    FEDDLLEGKHGLX
a277        FEDDLLEGKHGLX
              250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1  ttgctgcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaaat acggccggta
151 caggtaaccg tgcgccttc tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gactcgcgct ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgta tagtcgtgta
451 caaagcactc agtttgctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1  LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1  TTGCGCGCAA TCACGCCCCG TGCGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CCGCTCCGAC CAGTTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GCGGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1  LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPOVRTSFT DRFSILALIK SLISAGLSM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDL DRDFQLAVET LIQHLHQLAD
201 LFVGQRIGTV NDRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVTVSPSLIC				
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
m278	SYPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGLS	CMKTLIRHSRVQSTQFALYRQIQNLITHFNF				
m278	DRFSILALIKSLISAGLS	CMKTLIRHSRVQSTQFALYRQIQNLITHFYAANQLRFDF				
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFV	QGQRIGTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

```

1   TTGCGCGCAA TCACGCCCGG TCGGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCGAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTT GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1   LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QTVSPSLIC SCSPTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLMC				
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVTVSPSLIC				
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
a278	SCSPNTTAPTESRSRFIAKPKVLP	GNSSISPCIASDKPWMRTIPSVTEITVPRVLTSAFT				
	70	80	90	100	110	120

	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLS	CMKTLIRHSRV	QGTQFALYRQIQ	NLITHFNFYA	ANQLR	EDF
a278	DRFSILALIKSLISAGLS	CMKTLIRHSRV	QGTQFALYRQIQ	NLITHFNFYA	ANQLR	EDF
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHL	HLQADLFV	QGRI	GTVNDGR	FDMVEX	
a278	DRDFQLAVETLIQHL	RLQADLFV	QGRI	GTVNDGR	FDMVEX	
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

q279.seq

1	atgacgcgga	tttgcggctg	cttgatttca	acggttttga	gtgtttcggc
51	aagtttgtcg	gcggcggggt	tcatacaggct	gcaatgggaa	ggaacggata
101	ccggcagcgg	cagggcgcgt	ttggctccgg	cttctttggc	ggcagccatg
151	gtgcgtccga	cggcgcgggc	gttgctgca	atcacgactt	gtccggggcg
201	gttgaagttg	acggcttcga	ccacttcgcc	ctgtgcggat	tcggcacaaa
251	tctgcctgac	ctgttcattc	tccaaaccca	aaatggccgc	cattgcgctt
301	acgccttgcg	gtacggcgga	ctgcatcagt	tcggcgcgca	ggcggacgag
351	tttgacggca	tcggcaaaat	ccaatgcttc	ggcggcgaca	agcgcggtgt
401	attcgccgag	gctgtgtccg	gcaacggcgg	caggcgatctt	gccgcccaat
451	tccaaataag				

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

q279 . pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

1	ATAACGCGGA	TTTGC GGCTG	CTTGATTTC A	ACGGTTTTTC A	GGGCTTCGGC
51	AAGTTTGTCG	GCGGCGGGTT	TCATCAGGCT	GCAATGGGAA	GGTACGGACA
101	CGGGCAGCGG	CAGGGCGCGT	TTGGCACCGG	CTTCTTTGGC	GGCAGCCATG
151	GCGCGTCCGA	CGGCGGCGGC	GTTGCCTGCA	ATCACGATTT	GTCCGGGTGA
201	GTTGAAGTTG	ACGGCTTCGA	CCACTTCGCT	TTGGGCGGCT	TCGGCACAAA
251	TGGCTTTAAC	CTGCTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	GGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	TCAATGCGCC	GGCGGCAACG	AGTGCGGTGT
401	ATTGCCCGAG	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCTAAATAG				

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	: : : : : : : : : : : :					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120


```
a279.seq
1  ATGACNCNGA TTTGCGGGCTG CTTGATTTCA ACGGTTTNNA GGGCTTCGGC
51  GAGTTTGTCG GCGGCGGGTT TCATGAGGCT GCAATTGGGA GGTACNGACA
101 CNGGCAGCGG CAGGGCGCGT TTGGCGCCGG CTCCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGC ATTGCTTGCA ATCACGACTT GTCCGGCGGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAA
251 TTTGTTTTCAC CTGTTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCCGT
451 TCCGAATAG
```

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	<u>ARSTAAALPA</u>	<u>ITTCPGELKL</u>	<u>TASTTSSCAD</u>	<u>SAQICFTCSS</u>	<u>SKPRIAAIAP</u>
101	<u>TPCGTADCIS</u>	<u>SARXRTSLTA</u>	<u>SAKSNAPEAT</u>	<u>SAVYSPXLCP</u>	<u>ATAAGVLPPA</u>
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:					
a279	MTXICGCLISTVXRASASLSAAGFMRLQEWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSRRLCPATAAGVLFPASKX					
a279	SAKSNAPAATSAVYSPXLCPATAAGVLFPASEX					
	130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakvi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaaccttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgcgcgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgcaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgccc aaa acgtcgctga aacctgata aaggccgac cgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaagcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtccctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaaacaagt cgccgccatc atccggcaaa tcaaacgcga aggcacaaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcacgc
801 caaagaaacc ggcgtaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EEGGHHHDH HDHDHDHEGH HHDHGEYDPH VWNDFVLMDS
151 YAQNV AETLI KADPEGKVY QORLGNYQM LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251 AVFTENIKDT RMDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACCTCAC CCTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGCTCAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GGCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EEGGHHHDH HDHEGHHHDH GEYDPHVWND PVLMSAYQON
151 VAKALIKADP EGKVYQQL GNYQMQLKKL HSDAQAAFNA VPAKRKVL

```

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAAIIRQI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng)
 from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTLIAALLTASATAAPLPVVTFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTLIAALLATAATAAPLPVVTFSILGDVAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDH-					
	:					
g280	TSGDIKKIRSAKLVLLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQQLGNYQMQ					
	:					
g280	HDHDHDHEGHHHDHGEYDPHVWNDPVLMSDYAQNVAETLIKADPEGKVYYQQLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI					
	:					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSSAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	:					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNVE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
51	AACTGCCGCC	CCCCTGCCGG	TTGTAACCAG	CTTCAGCATT	TTAGGCGACG
101	TAGCCAAACA	AATCGGCGGA	GAGCGCGTAT	CCATACAAAG	TTTGGTCGGA
151	GCCAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGGCG	ACATTAAAAA
201	AATCCGCAGT	GCAAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
301	ACCAAAGGCA	TCCAACCCCT	CAAAGCCGAA	GAAGAAGGCG	GACACCATCA
351	CGACCACGAT	CATGACCACG	ACCATGACCA	CGAAGGACAC	CACCACGACC
401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCTT	TATGTCCGCC
451	TATGCCCAAA	ACGTGCGCGA	AGCCCTGATA	AAGGCCGACC	CCGAAGGCAA
501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCCTGC	CGCCAAACGC
601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
701	CCAAACAAGT	CGCCGCCATC	ATCCGACAAA	TCAAACGCGA	AGGCATCAAA
751	GCCGTATTTA	CCGAAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGC

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801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHKPLTLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDEGH HDHGEYDPH VWNDPVLMSA
 151 YAQNVAEALI KADPEGKVYY QORLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTHGDAFS YMGKRYHIEF IAPQGSSEA EPSAKQVAI IRQIKREGIK
 251 AVFTENIKDT RMVDRIAKET GVNVSGLYS DALGNAPADT YIGMYRHNK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

m280.pep	10	20	30	40	50	60
	MKHLKLTLIAALLTASATAAPLPVVTFSISILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
a280	MKHKPLTLIAALLTTAATAAPLPVVTFSISILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	10	20	30	40	50	60
m280.pep	70	80	90	100	110	120
	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280	TSGDIKKIRS AKLVLLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE EGGHHHDHD					
	70	80	90	100	110	120
m280.pep	130	140	150	160	170	
	HDH---EGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
a280	HDHDHDEGHHDHGEYDPHVWNDPVLMSAYAQNVAEALIKADPEGKVYYQORLGNYQMQ					
	130	140	150	160	170	180
m280.pep	180	190	200	210	220	230
	LKKLHSDAQA AFNAVPAAKRKVLTHGDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAI					
a280	LKKLHSDAQA AFNAVPAAKRKVLTHGDAFSYMGKRYHIEFIAPQGSSEA EPSAKQVAI					
	190	200	210	220	230	240
m280.pep	240	250	260	270	280	290
	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
a280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	250	260	270	280	290	300
m280.pep	300					
	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcatc cgtcttctgc ctgtccctca gcgcgcacc
 51 cgctggcgta ttctcgta tgcgcgat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgcccgcg tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtggcgggg tttgcccgcg gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctt caagtccgct aacggcaaag gcgggctttg

```

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccgtt tatgggcaag aaatatgggg acgctcattc tgttgccgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgag cgctctttat
751 cttttttccg tcatactcgg caaagaaggc ggcattctgc ccaaattggtt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC  LSLSAAPVGV  FLVMRRMSLI  GDALSHAVLP  GAAVGYMFAG
51  LSLPAMGVGG  FAAGMLMALL  AGLVSRFTTL  KEDANFAAFY  LSSLAIGVIL
101 ISKNGSSVDL  LHLLFGSVLA  VDIPALQLIA  AVSGLTLITL  AVIYRPLVLE
151 SIDPLFLKSV  NGKGGWLWHVI  FLVLVVMNLV  SGFOALGILM  SVGIMMLPAI
201 TARLWARNMG  TLILLSVLI  LFCGLIGLLI  SYHIEIPSGP  AILCCSVLY
251 LFSVILGKEG  GILPKWFKNH  RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG  CCCTCGCATC  CGTCTTCTGC  CTGTCCCTCA  GTGCCGCACC
51  CGTCGGCGTA  TTCCTCGTCA  TGCGCCGTAT  GAGCCTGATA  GGCGACGCAT
101 TGAGCCACGC  CGTCCTGCCC  GGTGCCGCCG  TCGGCTACAT  GTTTGCCGGC
151 TTGAGCCTGC  CCGCCATGGG  TTTGGGCGGC  GTAGCCGAG  GCATGCTGAT
201 GGCACGTGCTT  GCCGGACTCG  TCAGCCGCTT  CACCACCCTG  AAAGAAGATG
251 CCAACTTTGC  CGCCTTTTAT  CTCAGCAGCC  TCGCCATCGG  CGTAGTCCTC
301 GTCAGCAAAA  ACGGGAGCAG  CGTCGATTG  CTCCACCTCC  TTTTCGGCTC
351 TGTACTTGCC  GTCGATATTC  CTGCCCTGCA  GCTCATCGCC  GCCGTCTCCA
401 GCCTCACGCT  CATTACCCTT  GCCGTCTATCT  ACCGCCCGCT  CGTACTCGAA
451 AGCATCGACC  CCCTGTTTCT  CAAATCCGTC  GGCGGCAAAG  GCGGGCTTTG
501 GCACGCTCTC  TTTCTCGTCC  TGGTCGTCAT  GAACCTCGTA  TCCGGCTTTC
551 AAGCCCTCGG  CACACTCATG  TCCGTCGGAC  TCATGATGCT  GCCAGCCATT
601 ACCGCCCGCC  TGTGGGCGAA  GCATATGGGC  GCACTCATCC  TCCTATCCGT
651 TCTGACAGCC  CTGCTGTGCG  GCTTGAGCGG  ACTGCTCATT  TCCTACCACA
701 TCGAAATTCC  TTCCGGTCCC  GCCATCATCC  TCTGTTGCAG  CGTCTTTTAT
751 CTCTTTTCCG  TCATACTCGG  CAAAGAAGGC  GGCATTCTGA  CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC  LSLSAAPVGV  FLVMRRMSLI  GDALSHAVLP  GAAVGYMFAG
51  LSLPAMGLGG  VAAGMLMALL  AGLVSRFTTL  KEDANFAAFY  LSSLAIGVVL
101 VSKNGSSVDL  LHLLFGSVLA  VDIPALQLIA  AVSSLTLITL  AVIYRPLVLE
151 SIDPLFLKSV  GGKGGWLWHVL  FLVLVVMNLV  SGFOALGILM  SVGLMMLPAI
201 TARLWAKHMG  ALILLSVLTA  LLCGLSGLLI  SYHIEIPSGP  AILCCSVLY
251 LFSVILGKEG  GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

```

          10          20          30          40          50          60
m281 . pep  MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGLGG
          | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||
g281        MHYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGVGG
          10          20          30          40          50          60

          70          80          90          100         110         120
m281 . pep  VAAGMLMALLAGLVSRTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g281        FAAGMLMALLAGLVSRTTLKEDANFAAFYLSSLAIGVILISKNGSSVDLLHLLFGSVLA
          70          80          90          100         110         120

          130         140         150         160         170         180
m281 . pep  VDIPALQLIAAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGWLWHVLFLVLVVMNLV

```

640

```

g281      |||||:|||||:|||||:|||||:|||||
          130      140      150      160      170      180
          190      200      210      220      230      240
m281.pep  SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP
          |||||:|||||:|||||:|||||:|||||:|||||
g281      SGFQALGILMSVGIMMLPAITARLWARNMGTLLILLSVLIALFCGLIGLLISYHIEIPSGP
          190      200      210      220      230      240
          250      260
m281.pep  AIILCCSVLYLFSVILGKEGGILT
          |||||:|||||:|||||:|||||
g281      AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX
          250      260      270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

```

a281.seq
1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51 CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCACGTGCTT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 CGTACTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GGCGGCAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CCAAATGGCT
801 CAAAACCAC CGCCACCACA CCACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

```

a281.pep
1  MRYALASVFC LSLSAAPGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSTLTLLTL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGTLM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLTAL LCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILTKWLKNH RHHTT*

```

m281/a281 99.2% identity in 264 aa overlap

```

          10      20      30      40      50      60
m281.pep  MRYALASVFC LSLSAAPGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG
          |||||:|||||:|||||:|||||:|||||:|||||
a281      MRYALASVFC LSLSAAPGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG
          10      20      30      40      50      60
          70      80      90      100     110     120
m281.pep  VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLLFGSVLA
          |||||:|||||:|||||:|||||:|||||:|||||
a281      VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLLFGSVLA
          70      80      90      100     110     120
          130     140     150     160     170     180
m281.pep  VDIPALQLIA AVSSLT LITLAVIYRPLV LESIDPLFLK SVGGKGLWHV LFLVLVVMNLV
          |||||:|||||:|||||:|||||:|||||:|||||
a281      VDIPALQLIA AVSTLT LLLTAVIYRPLV LESIDPLFLK SVGGKGLWHV LFLVLVVMNLV
          130     140     150     160     170     180

```

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILT		KWLKNRHHHTTX			
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 tttgggcatc agcgtcggtt cgtttcaggt cggcggcggg attttgggtg
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacgggggcaa gcgcgccccg cccgcaatgc
351 aggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcgggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttggtta
501 tgccatttta atcggttgcg ggaagggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattcccgc aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKO
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKO
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMMLAAVS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRLI					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRLI					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMMMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMMMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

1	ATGGGATTGG	GCATGGAAAT	CGGCAAGCTG	ATTGTGGCCTT	TTTTGGTGCT
51	GATTAATCCG	TTTAGCGCGT	TGTCGCTTTA	CCTTGACCTG	ACCAACGGGC
101	ACAGCACGAA	GGAGCGCAGG	AAGGTCGCGC	GGACGGCCGC	CGTTGCCGTG
151	TTTGCCGTGA	TTGCGGTATT	TGCGCTGATC	GGCGGTACGC	TGCTGAAGGT
201	TTTGGGCATC	AGCGTCGGTT	CGTTTCAGGT	CGGCGGCGGA	ATTTTGGTGT
251	TGCTGATTGC	CATTTTCGATG	ATGAACGGCA	ACGACAATCC	CGCCAAGCAG
301	AATCTCGGCG	CGCAGCCGGA	AACGGGGCAG	GTGCGCCCCG	CCCGCAATGC
351	CGGAGCGATT	GCCGTCGTGC	CCATCGCCAT	ACCGATCACC	ATCGGCCCCG
401	GCGGTATTC	GACCGTGATT	ATTTACGCTT	CGGCGGCTAA	AACATACGGC
451	GACATCGCGT	TGATTATCGC	AGCCGGTTTG	GTGGTCAGTG	CGATTTGTTA
501	TGCCATTTTA	ATCGTTGCCG	GGAAGGTCAG	CCGCCTGCTG	GGTGCGACGG
551	GGCTGACGAT	TTTAAACCGT	ATCATGGGTA	TGATGCTGGC	GGCGGTATCG
601	GTGGAGATTA	TTGTGTCGGG	ACTGAAAATG	ATATTCCCGC	AACTGGCAGG
651	TTGA				

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

1	MGLGMEIGKL	IVAFLVLINP	FSALSPLYDL	TNGHSTKERR	KVARTAAVAV
51	FAVIAVFALI	GGTLLKVLGI	SVGSFQVGGG	ILVLLIAISM	MNGNDNPAKQ
101	NLGAQPETGQ	VRPARNAGAI	AVVPIAIPIT	IGPGGISTVI	IYASAAKTYG
151	DIALIIAAGL	VVSAICYAIL	IVAGKVSRLI	GATGLTILNR	IMGMMMLAAVS
201	VEIIVSGLKM	IFPQLAG*			

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGOVRPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPFIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPFIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1   atgaactttg ctttatccgt catcacattt accctcgcct ctttcctgcc
51  cgtcccgccg gccggaaccg ccgtctttac ttggaaagac ggccgaggca
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaataca
401 ataacgccgt aaacaaatac tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1   MNFALSVITF TLASFLEVPVP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTLQTKP AVKPKPAVDT NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1   ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGC CGGATTTCAA AAATGAACCT
351 GAAGCGGTG GAAATTCAA ATGCAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1   MNFALSVIML TLASFLEVPVP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTQTQKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLEVPVPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	: : : : :					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		:	:	:	:	:
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNNAVNKYCRX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1173>:

```
a283.seq
1  ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCG
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCAGCA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAAAGTGC CGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1174; ORF 283.a>:

```
a283.pep
1  MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAIE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*
```

m283/a283 100.0% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQIILNLRTQTKP					
a283	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQIILNLRTQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
a283	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNNAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNNAVNKYCRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1175>:

```
g284.seq.
1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51  aggttggggc ttagcggctt ttgtaacggc attcgctttt gcctgcacaaa
101 gactgcgcgg ctttgcgttt gcctttgaag ccttcgcggg tttttttgaa
151 actgtctttc ttaaagcctt ctttcttgaa accttcgcgg cgcgttttgc
201 cgccgaagcc ttctttgccc ggtttatgat cgccgcgcgg gccgcgggat
251 ttcctatcgc ccagcgcggc ttgaccttgc ggcttgccgc ctgcggattt
301 gcgtttgcgg gccggctcca tgccttcgat ggtcagttcg ggcagtttgc
351 ggttaatgta tttttcgatt ttgtggactt tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgg tgcgccgat
451 gcgggtggacg tagtcttccg cctgtttcgg caggtcgtag tttatgacgt
```

```

501  gggtaatggt  cggtagctca  ataccgcgtg  cggcaacgtc  ggtggcaacc
551  aaaattttgc  agcggccttt  acgcaaattc  gtcagcgtgc  ggttgcgcca
601  gccctgcggc  atatcgccgt  gcaggcagtt  gccggcgaaa  cctttttcgt
651  acaattcatc  cgcgatgact  tcggatcatc  ctttggtgga  cgtgaaaatc
701  acacattggt  cgatgttggc  atcgcgcagg  atgtggtcga  gcaggcggtt
751  tttgtggcgc  atatcgtcgc  agtacaacaa  ctgctcttcg  attttgcctt
801  ggccgtccac  gcgttcgact  tcgataattt  cagagtcctt  ggtcagtttg
851  cgcgccagtt  tgccgactgc  gccgtcccaa  gtggcggaga  acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

g284.pep

```

1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51  TVFLKAFFLE TFAARFAAEA FFARFMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGKRNNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVGNNG RYVNTACGNV GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHRFGG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LLFDLALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

m284.seq..

```

1  ATGCCGCTCTG AAACGCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTGTGAA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTGC
201 CGCCGAAGCC TTCTTTGCTC GGTTCATGAT CGCCGCGCCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGCGG GTCGGTTCCA TGCCTTCGAT GGTCAATTTC GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCAGCCT GCGCGGCCGG TCGCGCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTTCGTAG TTGATAACGT
501 GGGTAATGGT CGGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAAATTTTG AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTTCGCGCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TCGCGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGGG CGTGAAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATTT CAGGGTCTTT GGTCACTTTG
851 CGCGCCAGTT TGCCGACCGC GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGCGGTTG CTTCCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAAA
1001 CGTTCAAAAT CAACTTTGCC GCTTTGCATC AGGTCCATCA GACGGCCCCG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGGCATACG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGGCCTTT GCCCGGTTTT TCCTGCGGTT
1251 TGGTCAGTTT TTGCAAAGTC GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

m284.pep

```

1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51  TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFLHAFD GQFGQFSVNV FFDFVDFDVF VHFGKRNNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNNGNG RYVDTACGNI GGNQNFAAAF TQIRQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFGG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVNQ HFQTFKINFA ALHQVHQTAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

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	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQGQFQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAGRLHAFDQGQFQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVHFGKRNTRACAAGAPDAVDVVERLFRQVVVDVNGRNVDTACGNI					
g284	FFDFVDFDVHFGKRNTRACAAGAPDAVDVVERLFRQVVVDVNGRNVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRRFGGRENHTLVVVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDFDVVDKAHIQHTVGFVQNHQFQTFKINFALHQQVHTARRGDNQIDREA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGCTCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101  GAATCGCCGG  CTTTGCGTTC  GCCTTTGAAG  CCTTCGCCGG  TTTTGTGAA
151  ACCGCTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTC
201  CGCCGAAGCC  TTCTTTGCTC  GGTATTATGAT  CGCCGCGCCA  ACCGCGCGAT
251  TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301  GCGTTTTCGG  GTCGTTTCCA  TGCCTTCGAT  GGTGAGTTTC  GGCAGTTTTC
351  GGTAAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401  GCAAACGTAA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TCGCGCCGAT
451  GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501  GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551  AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601  GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GGCGGCGAAA  CCTTTTTCGT
651  ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701  ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751  TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801  GGTGCTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTGAGTTTG
851  CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901  CTGACGGTCT  TCCGGCGTGG  CTTTCGACGAT  GGTTCGATG  TCGTCGATAA
951  AGCCCATATC  CAACATACGG  TCGGCTTCGT  CAAAATCAG  CACTTCCAAG
1001  CGGGCGAAAT  CGACTTTGCC  GCTTTGCATC  AAGTCCATCA  GACGCCCCGG
1051  CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101  CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151  TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201  CGGCGTCAAC  ACCAACGCGC  GCGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251  TGGTCAGTCG  CTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

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```

51 TVSLKAFFLE TFAARFAAEA FFAREFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRHFHAFD GQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRFLR QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGFGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQV FLDLSRQFAG
401 RRQHQRRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

```

              10      20      30      40      50      60
m284.pep      MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              |||||
a284           MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE
              10      20      30      40      50      60

              70      80      90      100     110     120
m284.pep      TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              |||||
a284           TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV
              70      80      90      100     110     120

              130     140     150     160     170     180
m284.pep      FFDFVDFDVFVHFGKRNRTAACAAGAPDAVDVFRFLRQVVVDNVGNRYVDTACGNI
              |||||
a284           FFDFVDFDVFVHFGKRNRTAACAAGAPDAVDVFRFLRQVVVDNVGNRYVDTACGNV
              130     140     150     160     170     180

              190     200     210     220     230     240
m284.pep      GGNQNFAAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG
              |||||
a284           GGNQNFAAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGFGGRENHALIDVG
              190     200     210     220     230     240

              250     260     270     280     290     300
m284.pep      IAQDMIEQAVFVAHIVAVQQLFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
              |||||
a284           IAQDMIEQAVFVAHIVAVQQLFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS
              250     260     270     280     290     300

              310     320     330     340     350     360
m284.pep      LTVARRCFHDGFDVVDKAHIQHTVGFVQNGHFQTFKINFAALHQVHQTARRGDNQIDRFA
              |||||
a284           LTVFRRGFDDGFDVVDKAHIQHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA
              310     320     330     340     350     360

              370     380     390     400     410     420
m284.pep      QGTGLVAERRAADDADGAEPHTHIFGIRQVFLDLSRQFAGRGQHSTRAFARFFAAGQF
              |||||
a284           QGAGLVAERCTTDDADGTEPHTHIFGIRQVFLDLSRQFAGRRQHQRRARAFARFFAAGQS
              370     380     390     400     410     420

m284.pep      LQSRX
              ||||
a284           LQSRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1  atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcgcg gcactgctgt ctgtcctgat tttggcagta

```

151 tgttttctctg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201 gtaccaaatac ccgtcctggt tcggcgtaaa catcttctcc caaaacctca
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301 gagggggcag accttaaaat cagccgcttc cgcttcgcgt ggaaaccgtc
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401 tcgccatcgt aaccaaaccg actccgccta aagaagaacg ccgcctcaa
451 ggcctgcccg acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacctgtc
551 atctcgaacg cctcaacgcg gcataccgtt acgaccgtaa agggcaccgc
601 ctcgacctga aggccgcga cagccgtg agcagttcgt cggggtcagc
651 ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701 aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcggc
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801 cctctcggga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901 gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgcatccc
951 gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttggaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tccccgtccg tcaggttttg
1051 ggcggttttg tcatccggca ggacggcacg gtgcataatc gcaatacgtc
1101 cgccgccctg ctcggacggg gcggcatcag gctgtcgggc aaaaatcgaca
1151 ccgaaaaaga catccttgat ttaaataatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacgc gttcaaaagg aggttgagcg gcagcatcgg
1251 catcggcgcc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg
1301 gacggcacg cacggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtggt cgacacggtc aacatctccg ccggggaagg
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1501 tttccggcag gcaatatcaa cggttcgatt catcttgccg gtgaactggc
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1651 ccgcgcgccg ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
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1751 ccgatttate ccgtttcggc ttcggactcg cggggtcttt aaatgtacgc
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2001 tgtcgatacc gccggcctga cgctggaagg tacggggcgcg cagcaccgca
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2101 ttggacgctt caggcgccat caacaggga cttaccgat ggaaggcag
2151 catcggcatc ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcgggcaag tgcggcaaat
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2301 gaaaaccggc atatcgga aaggcgggcg acgcgccctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccctcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgctta cgggcacaaac gcgcggcggt acctcaatat
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2851 accgcacctt tggcgggcag gctcaacctg accgttgccg atgccgaagc
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2951 ccgccgtaac cctcggcggc agcatcgccg acccgcaact gggcggcagt
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3051 ggacaacggc tcgctgcgtt cgcataattg aggcaggaaa tgggtaatcg
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3151 agcatggaaa acagcgtgcc cgatgtcgat atcggcgcgg tgttcgacaa
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3251 ccgcctgctg ctattcgccg caaaaaggca tatccgttac cggatgatt
3301 aaaactgatc agggcggtt cggttcgcaa aaatcctcga tgccgtccgt
3351 cggcgacgat gtcgtcgat tgggcgaagt caagaaagag gcggcgcat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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3451 ttctccggct acggcgcgga cgttaccata ggccggcaaac tgaccctgac
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3551 aaggcggtta caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgtg caacgacccc aacctgaaca tccgcgcga
3651 acgcccgcct tccccgcgtg gtgcggggcg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcggca gcagcggcg
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgacg
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

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This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

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1 MTDTTPDTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSLEL RRSLHITDIS AGDIAIVTKP TTPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGTDFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRALT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGLT AQGYLELFKD RLLKLDIRS AFDPSTRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTGGGF GKKGDRNLNL ITAPDLRFRG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG TARNLHIGKA ADIRSLDFTL KGSFGTSRPM
651 RADIKGGRLS LSGGAHVVD AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PFEHNLVLN
801 GDWDVAYGHN ARGYNISRQ SGDAVLPGGQ ALGLNAFLSK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNTGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD
951 TAPLGGRNLN TVADAEAFRN FLPVGTQVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPDVG IGAVFDPKYRI LSRPNRLTV SGNTRLRYSK QKGISVTGMI
1101 KTDQGLFGSQ KSSMPVGGD VVVLGEVKE AAASLPVNMN LTDLDNGIR
1151 FSGYGADVTI GSKLTTLTAQF GGNVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEFMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFLGSDKK DSAGNGK GK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

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1 ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCG
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAAA CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTC GCCGCGGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCCTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGCGGCG
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
 901 GTGCCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
 951 GTCGTTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAACA
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA
 1051 GCGGGCTTTG TCATCCGGCA GGACGGCAGG GTGCATATCG GCAATACGTC
 1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCCGGC AAAATCGACA
 1151 CCGAAAAAGA CATCTCGAT TTAATATAG GCATCAACTC CGTCGGCGCG
 1201 GAAGACGTAC TGCAAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
 1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCCGGCATCG
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
 1451 AGCTGGACAT CCGTTCCCGC GCATTCGACC CTTCCGCGAT CGATCCGCAA
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAAGTGGC
 1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
 1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
 1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA
 1701 CCGCGGCTTC GCGAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCACAC
 1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
 1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
 1851 CTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTCCG CCGACACAAG CCGCCCGATA
 1951 CCGCGCGACA TCAAAGGCAG CCGCCTTTCG CTGTCCGGCG GAGCGCGGT
 2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
 2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCGAG
 2151 CATCGGCATC CTCGACATCG GCGGCGCAT CAACCTCAAG CTGCAAAACC
 2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGCGGCAAG TGCGGCAAT
 2251 TGGCAGGCAA TGGGCGGCG CTTCAACCTG CAACACTTTT CTGGGATAA
 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
 2351 AGTTGCACAA TTTCTTCAA CCGCCTTCG AACACAATCT GGTTTTAAAC
 2401 GCGGACTGGG ATGTCGCCTA CGGGCGCAAC GCGGCGGCT ACCTCAATAT
 2451 CAGCCGCAAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
 2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
 2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCCG ATTTGGGCAT
 2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
 2651 TTACCGCCTC CTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
 2701 GCGGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGCGG
 2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
 2801 ACGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
 2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
 2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
 2951 CCGCGTAAC CCTCGGCGG AGCATCGCCG ATCCGCACTT GGGCGGACG
 3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
 3101 ACAGCCTGAA ATTCGGGCAC GAAGGGACGG CGGAACCTCT CCGGTACGGTC
 3151 GGTATGGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTGACAA
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
 3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCCGTTAC CGGGATGATT
 3301 AAAACGGATC AGGGGCTGTT CGGTTTCGAA AAATCCTCGA TGCCGTCCGT
 3351 CCGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
 3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
 3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCTGAC
 3501 CGCCAATCG GCGGAAGCG TACGGGCGGT GGGCACGGTC CGCGTCATCA
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
 3601 GTCTCCTTTG TCGGCGCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
 3651 ACGCGCCTT TCCCCGTCG GTGCGGGCGT GGAAATATG GGCAGCCTCA
 3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAAAAGAC
 3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
 3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAAATCA
 3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
 3901 CGCAACGCGC AAACGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT
 3951 CGGCAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
 4001 CCAGCGCGGA ACAGTCCGTC AAATGATTT ACCGGCTGAC CCGCGCCATA
 4051 CAGGCGGTTG CCGGTATCGG CAGCGGTTTCG TCGGCGGCG AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep
 1 MTDAPTDTPTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
 51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRFR FAWKPSSELM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
 151 SLPDSIDLPA AVYLDRLFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
 301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RNGIPVRQVL
 351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSPRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIKTG DGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
 601 GHLSGDLDDG IRTFETDLSG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGA AVVD T ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSNLN QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
 851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFPLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSR SFD
 951 TAPLGGRLNL TVADA EVFRN FLVPVQTVKG SLNAAVTLGG SIADPHLGGS
 1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLYRSP QKGISVTGMI
 1101 KTDQGLFGSQ KSSMP SVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
 1151 FAGYGADVTI GGKLTTLTAQS GGSVRGVGT VVIKGRYKAY GQDLDTKTGT
 1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
 1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
 1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNGKKGK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

m285.pep	10	20	30	40	50	60
	MTDTAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
g285	MTDTTPTDPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
m285.pep	70	80	90	100	110	120
	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRFAWKPSSELM					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
m285.pep	130	140	150	160	170	180
	RRLSHITEISAGDIAIVTKPTTPPKEERPPLSLPDSIDLPAAVYLDRLFETGKISMKGAFDK					
g285	RRLSHITDISAGDIAIVTKPTTPPKEERPQGLPDSIDLPAAVYLDRLFETGKISMGTFDK					
	130	140	150	160	170	180
m285.pep	190	200	210	220	230	240
	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
m285.pep	250	260	270	280	290	300
	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

a285.seq

1	ATGACCGATA	CCGCACCGAC	AGATACCGAT	CCGACCGAAA	ACGGCACGCG
51	CAAAATGCCG	TCTGAACACC	GCCCTACCCC	GCCGGCAAAA	AAACGCCGCC
101	CGCTGCTGAA	GCTGTCGGCG	GCATGCTGT	CTGTTCTGAT	TTTGGCAGTA
151	TGTTTCCTCG	GCTGGCTCGC	CGGCACGGAA	CGGGTTTTCG	GCTTCGGGCT
201	GTACCAAATC	CCGTCTTGGT	TCGGCGTAAA	CATTTCTCTC	CAAAACCTCA
251	AAGGCACGCT	GCTCGACGGC	TTCGACGGCG	ACAACCTGGT	GATAGAAACC
301	GAGGGGGCAG	ACCTTAAAA	CAGCCGCTTC	CGCTTCCGGT	GGAAACCGTC
351	CGAAGTGATG	CGCCGACGC	TGCACATTAC	CGAAATTCTC	GCCGGCGACA
401	TCGCCATCGT	TACCAAACCG	ACTCCGCCTA	AAGAAGAACG	CCCGCCGCTC
451	AGCCTTCCCG	ACAGCATAGA	CCTGCCTGCC	GCCGTCTATC	TCGACCGCTT
501	CGAGACGGGC	AAAAACAGCA	TGGGCAAAAG	CTTTACGAAA	CAAACCGTCT
551	ATCTCGAACG	GCTGGATGCT	TCATACCGTT	ACGACGACAA	AGGACACCGC
601	CTCGACCTGA	AGGCTGCCGA	CACGCCGTGG	AGCAGTTTCG	CGGGGTTCAG

651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCTTTC
901 GTGCCCTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGCTCCG TCAGGTTTAA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTGCGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCGCGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCGCCG GCATTCGACC CTTCGCGCAT CGATCCGCAA
1501 TTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGGCG GCGAACTGGC
1551 AAAAGAGAAA TTACACAGCA AAATGCGGTT TTTACCGGC ACGTTCACCG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA
1701 CGGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAGCA
1751 CCGATTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
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3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACCGCG AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCGGTATCGG CAGCGGTTTC TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
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101 EGADLKISRF RFAWKPELMM RRLSHITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPFSF DGIALEGSLD LENTKAGFAD RNGIPVRQVL
351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSST AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTGDDG GKKGDRNLNL ITAPDLRSFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLGG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDT ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSGIG LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSNLN QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFLPA
901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSEF
951 TAPLGGRLNL TVADADEVFN FLPVGTQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRENRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GCKLTTLTAQS GGSVRGVGTV RVIKGRYKAY QODLDITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA QINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNSKKG*

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m285/a285 99.4% identity in 1389 aa overlap

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a285           MTDAPTDTPTDPTENGTRKMPSEHRPTPPAKKRRPFLKLSAALLSVLILAVCFLGWLAGTE
              10      20      30      40      50      60

              70      80      90      100     110     120
m285.pep      AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPELMM
              |||||
a285           AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPELMM
              70      80      90      100     110     120

              130     140     150     160     170     180
m285.pep      RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK
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a285           RRLSHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLDRFETGKISMKGAFDK
              130     140     150     160     170     180

              190     200     210     220     230     240
m285.pep      QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
              |||||
a285           QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
              190     200     210     220     230     240

              250     260     270     280     290     300
m285.pep      TIHSTARLSGSLKDVRAELIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
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656

a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF
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a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRF LPCTFNGVPIAGS
a285	RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRF LPCTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLN LNITAPDLSRFGFGLAGSLNVR
a285	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRLN LNITAPDLSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDL DGGIRTFFETDL SGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
a285	GHLSGDL DGGIRTFFETDL SGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGA VVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
a285	LSGGA EVVD TADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
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	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLP GGQALGLNAFSLK
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	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGTLKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYGKINGNITV GQSRSFDTAPLGGRINL

657

a285	AAQNITGSLNAAQIGGRVGS	SPSVNA	AVNGSS	NYGKING	NITVGQ	SRSFDTAP	LGGR	LNL
	910	920	930	940	950	960		
m285.pep	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGS	ADPH	LGGS	INGDKLYRNQ
a285	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGS	ADPH	LGGS	INGDKLYRNQ
	970	980	990	1000	1010	1020		
m285.pep	SLRSHIAGRK	WVIDSL	KFRHEG	TAE	LSGT	VMEN	SGPD	VDIGAVFDKYRILSRPNRRLTV
a285	SLRSHIAGRK	WVIDSL	KFRHEG	TAE	LSGT	VMEN	SGPD	VDIGAVFDKYRILSRPNRRLTV
	1030	1040	1050	1060	1070	1080		
m285.pep	SGNTRLRY	SPQKGI	SVTGM	IKTDQ	GLFG	SQKSS	MP	SVGDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRY	SPQKGI	SVTGM	IKTDQ	GLFG	SQKSS	MP	SVGDDVVVLGEVKKEAAAPLPVNMN
	1090	1100	1110	1120	1130	1140		
m285.pep	LTLDLNDG	IRFAGY	GADVT	IGGK	LTLTAQ	SGGS	VRGV	GTVRVIKGRYKAYGQDLDTKGT
a285	LTLDLNDG	IRFAGY	GADVT	IGGK	LTLTAQ	SGGS	VRGV	GTVRVIKGRYKAYGQDLDTKGT
	1150	1160	1170	1180	1190	1200		
m285.pep	VSVFVG	PLNDP	NLNIRA	ERRLS	VPVAG	VEILG	SLNS	PRITLTANEP
a285	VSVFVG	PLNDP	NLNIRA	ERRLS	VPVAG	VEILG	SLNS	PRITLTANEP
	1210	1220	1230	1240	1250	1260		
m285.pep	GSGSSG	DNAALS	AAA	GALLAG	QINDR	IGLV	DDLG	FTSKRSRNAQTGELNPAEQVLT
a285	GSGSSG	DNAALS	AAA	GALLAG	QINDR	IGLV	DDLG	FTSKRSRNAQTGELNPAEQVLT
	1270	1280	1290	1300	1310	1320		
m285.pep	LTGKLY	IGYEYS	ISSAE	QSVK	LIYRL	TRAIQ	AVARIG	SRSSGGELTYTIRFDRFSGSDKK
a285	LTGKLY	IGYEYS	ISSAE	QSVK	LIYRL	TRAIQ	AVARIG	SRSSGGELTYTIRFDRFSGSDKK
	1330	1340	1350	1360	1370	1380		
m285.pep	DSAGNG	KGKX						
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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1   CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATT CTCCCCAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGGCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCTCT
701 CGGGAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTC AACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTGGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTGGGCGG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCGG
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1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
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3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
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3401 AACCAGGGCG AATGTGCGT GGGGTGGGCA CGGTCCGCGT CATCAAAGG
3451 CGTTACAAAG CATACGGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTGTTCGGC CCGCTCAACG ACCCCAACCT GAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCGC CCTCAACAGC
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3651 CTCCTGGCTC ATCTCAACC GTGCCGGCAG CCGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCA GCGCGCTGCT TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GGCGAACCTA ACCCGCGCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACGTAC CCGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 CCGGAACAGT CCGTCAAAC GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGCGG CGGCGAGCTG ACATACACCA
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4051 GGCAAGGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep


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101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGfNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSILTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAG LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLG DLGGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGPSG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASAANWQAMG GSLNLQHSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGQALGLN
801 AFSKLRTRFQ DRIGILLDGG ARFGRINADL GIGNAFGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNLSAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRLNLTVADA EAFRNFLPVG QTVKGSLSNA
951 VTLGGSIA DP HLGGSSINGDK LYRNTQOGI ILDNGLSRSH IAGRKWVIDS
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1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAAASL
1101 PVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIK
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GK GK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

```

1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGCTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTG TTGGTTCCGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGTGCTCTG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAACAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGGC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGGCCG CCTTCGTGCC
801 TTTCCCTGCC GATGCCGGAC TGAATTTTGA CCTGACCGCC ATCCCGTCGT
851 TTTTCAGACG CATCGCGCTG GAAGGTTTCG TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTATC CGGCAGGACG GCACGGTGCA TATCGCAAT ACGTCCGCCG
1001 CCCTGCTCGG ACGGGCGGCG ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG CGCGGAAGA
1101 CGTACTGCAA ACCGCTTCA AAGGAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCAGC
1201 CCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GCATCCGTTT CCCGCGCAT CGACCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGCGCAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CGGATTGCGC GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TCCCGCCGTC GATTTCGCGC TGGGCGGAA CATTATTA AAACAGCGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGT GATTTCGACG GCGGCATCCG AACCTTGAA ACCGACCTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGCGCGCAGA CATCCGTTG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCGAC ACAAGCCGCC CGATACCGGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTG GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCGCA CCGATGCTG GACGGCACGG CCGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CATGACGCT GGATGGCAA CCGTCAAAT TCGATTGGA
2001 GCCTTCAGCG GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 CGATCCTCGA CATCGGCGGC GCATTCAACC TCAAGTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGCGG CAAATTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTTGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAGCGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GGCGGATTAA CGCCGATTTG GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCCG CGCGCAAATC GGCAGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CGGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT ATCGTCGCAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCGGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAAC
3201 GGATCAGGGG CTGTTCGGTT CGCAAAAATC CTGATGCGG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCCC
3401 AATCGGGGCG AAGCGTACGG GGCGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CCGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GGCGTGAAA TATTGGGCGC CCTCAACAGC
3601 CGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTTTGGCTC ATCTCAACC GCGCCGGCAG CGGCAGCAGC GGCAGCAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GCGCAACTCA ACCCGCGCA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCGCGC CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.psp

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1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDFGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLNTK
301 AGFADRNGIP VROVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDLLDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLSLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSREFGFLAG SLNVRGHLG DLDGGIRTFE TDLGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDTADLML DGTGVQHRIR
651 THAMTLDGK PFKFDLDASG GINRELTRWK GSGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRLNLTVADA EVFRNFLPVG QTVKGSLNAA
951 VTLLGSIADP HLGGSINGDK LYRNTQTQGI ILDNGLSLRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVMNMLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAQIIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 GK GK*

```

g285-1/m285-1 96.5% identity in 1354 aa overlap

10

20

30

40

50

60

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSFSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSFSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLNAAVTLGGSIADP					
m285-1	KINGNITVQSRSFDTAPLGGRLNLTVADAEVFRNFLPVGQTVKGSLNAAVTLGGSIADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTLTAPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTLTQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKGK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT  CGGCGGCACT  GCTGTCTGTT  CTGATTTTGG  CAGTATGTTT
51  CCTCGGCTGG  CTCGCCGCA  CGGAAGCGGG  TTTGCGCTTC  GGGCTGTACC
101  AAATCCCCTC  TTGGTTCCGC  GTAAACATT  CCTCCCAAAA  CCTCAAAGGC
151  ACGCTGCTCG  ACGGCTTCGA  CGGCGACAAC  TGGTCGATAG  AAACCGAGGG
201  GGCAGACCTT  AAAATCAGCC  GCTTCCGCTT  CGCGTGGAAA  CCGTCCGAAC
251  TGATGCCCGC  CAGCCTGCAC  ATTACCGAAA  TTTCCGCCGG  CGACATCGCC
301  ATCGTTACCA  AACCGACTCC  GCCTAAAGAA  GAACGCCCGC  CGCTCAGCCT
351  TCCCGACAGC  ATAGACCTGC  CTGCCGCCGT  CTATCTCGAC  CGCTTCGAGA
401  CGGGCAAAAT  CAGCATGGGC  AAAGCCTTTG  ACAACAAAC  CGTCTATCTC
451  GAACGGCTGG  ATGCTTCATA  CCGTTACGAC  CGCAAAGGAC  ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTTCA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTC CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCAAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGGCGACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 CGGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATC CGACCCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGGTC GATTTGCGGC TGGGGCGGAA CATTATTTAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGCGG GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTCT
1901 ATACCGCGCA CTTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGCG GGCAGCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGCGACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTCTC TCAAACCGCC CTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGCG GCGCGTTTCG GCGGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGCGCG CAGGATTACC
2551 CGCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGGCAAAATC GCGGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTTCGAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCGGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTG GACAAATACC
3101 GCATCTGTCT CCGCCCCAAC CGCCGCTTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAATAA
3201 GGATCAGGGG CTGTTTCGGT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATAAGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGG CCGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAG TATTGGGCG CTTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACC GCGCCGGCAG TGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGTC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAACC GGCGAACTCA ACCCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACGTAG CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 CGGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

a285-1.pep

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1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPD RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLGGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSNLQHFWSV DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLTVADA EVFRNFLPVG QTVKGSLNAA
951 VTLGGSIADP HLGGSSINGDK LYRNQTQGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLWL ILNRAGSGSS GDNAALSAAG GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRDFRFS GSDKKDSAGN
1351 SKGK*

```

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK					
m285-1	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	SLTAQGYLE	LFKDRLLK	LDIRSF	AFDPSRID	PQLPAGNINGS	INLAGE
m285-1	VLDTVNIAAGQGS	SLTAQGYLE	LFKDRLLK	LDIRSF	AFDPSRID	PQLPAGNINGS	INLAGE
	430	440	450	460	470	480	
a285-1.pep	490	500	510	520	530	540	
a285-1.pep	LAKEKFTG	KMRFLPG	TFNGVPI	AGSADIV	YESRHL	PRAAVDL	RRLGRNIIKTGGGFGKKGD
m285-1	LAKEKFTG	KMRFLPG	TFNGVPI	AGSADIV	YESRHL	PRAAVDL	RRLGRNIIKTGGGFGKKGD
	490	500	510	520	530	540	
a285-1.pep	550	560	570	580	590	600	
a285-1.pep	RLNLNITAP	DLRSRFG	FLAGSLN	VRGHL	SGDLGG	GIRTFET	DLSGAARNLHIGKAADIRS
m285-1	RLNLNITAP	DLRSRFG	FLAGSLN	VRGHL	SGDLGG	GIRTFET	DLSGAARNLHIGKAADIRS
	550	560	570	580	590	600	
a285-1.pep	610	620	630	640	650	660	
a285-1.pep	LDFTLKGS	PDTSRPI	RADIKGS	RSLSL	SGGA	AEVVD	TADLMLDGTGVQHRIRTHAAMTLDGK
m285-1	LDFTLKGS	PDTSRPI	RADIKGS	RSLSL	SGGA	AEVVD	TADLMLDGTGVQHRIRTHAAMTLDGK
	610	620	630	640	650	660	
a285-1.pep	670	680	690	700	710	720	
a285-1.pep	PFKFDL	DASGGIN	RELTRW	KGSIG	ILDIGG	AFNLK	LQNRMTLEAGAERVAASAANWQAMG
m285-1	PFKFDL	DASGGIN	RELTRW	KGSIG	ILDIGG	AFNLK	LQNRMTLEAGAERVAASAANWQAMG
	670	680	690	700	710	720	
a285-1.pep	730	740	750	760	770	780	
a285-1.pep	GSLNLQH	FSWDKKT	GISAKG	GAHGL	HIAELH	NFFKPP	FEHNLVLNGDWDVAYGRNARGYL
m285-1	GSLNLQH	FSWDKKT	GISAKG	GAHGL	HIAELH	NFFKPP	FEHNLVLNGDWDVAYGRNARGYL
	730	740	750	760	770	780	
a285-1.pep	790	800	810	820	830	840	
a285-1.pep	NISRQSG	DAVLP	GGQAL	GLNAF	SLKTR	FQNDRI	GILLDGGARFGRINADLDIGNAFGGNM
m285-1	NISRQSG	DAVLP	GGQAL	GLNAF	SLKTR	FQNDRI	GILLDGGARFGRINADLDIGNAFGGNM
	790	800	810	820	830	840	
a285-1.pep	850	860	870	880	890	900	
a285-1.pep	ANAPL	GGRITAS	LPDLG	TLPFL	PAAQ	NI	TGSLNAAQIGGRVGS
m285-1	ANAPL	GGRITAS	LPDLG	TLPFL	PAAQ	NI	TGSLNAAQIGGRVGS
	850	860	870	880	890	900	
a285-1.pep	910	920	930	940	950	960	
a285-1.pep	KINGNIT	VGQSR	SFDTAP	LGGRL	NLTVA	DAE	VRNFLPVGQTVKGS
m285-1	KINGNIT	VGQSR	SFDTAP	LGGRL	NLTVA	DAE	VRNFLPVGQTVKGS
	910	920	930	940	950	960	
a285-1.pep	970	980	990	1000	1010	1020	
a285-1.pep	HLGGS	INGDK	LYRNQ	TQGI	ILDN	GLRSH	IAGRKWVIDSLKFRHEGTAELSGTVGMENS
m285-1	HLGGS	INGDK	LYRNQ	TQGI	ILDN	GLRSH	IAGRKWVIDSLKFRHEGTAELSGTVGMENS
	970	980	990	1000	1010	1020	
a285-1.pep	1030	1040	1050	1060	1070	1080	
a285-1.pep	GPDVD	IGAVF	DKYRIL	SRPNR	RLTVS	GNTRL	RYSPQKGISVTGM
m285-1	GPDVD	IGAVF	DKYRIL	SRPNR	RLTVS	GNTRL	RYSPQKGISVTGM
	1030	1040	1050	1060	1070	1080	
a285-1.pep	1090	1100	1110	1120	1130	1140	
a285-1.pep	SVGDD	VVLGE	VKK	EAAAP	LPVNM	NLTLD	NDGIRFAGYGADVTIGGKLT
m285-1	SVGDD	VVLGE	VKK	EAAAP	LPVNM	NLTLD	NDGIRFAGYGADVTIGGKLT
	1090	1100	1110	1120	1130	1140	
a285-1.pep	1150	1160	1170	1180	1190	1200	
a285-1.pep	GVGT	VRVIK	GRYK	AYQD	LDIT	KGT	VSFVGPLNDPNLNIRAERRLS
m285-1	GVGT	VRVIK	GRYK	AYQD	LDIT	KGT	VSFVGPLNDPNLNIRAERRLS

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEPMSSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

g286.seq

1	atgcagaaca	ccggtaccat	gatgatcaaa	ccgaccgccc	tgctcctgcc
51	ggcttttattt	ttctttccgc	acgcatacgc	gcctgccgcc	gacctttccg
101	aaaacaaggc	ggcgggtttc	gcattgttca	aaagcaaaag	ccccgacacc
151	gaatcagtca	aattaaaacc	caaattcccc	gtccgcatcg	acacgcagga
201	cagtgaatc	aaagatatgg	tcgaagaaca	cctgccgctc	atcacgcagc
251	agcaggaaga	ggttttggat	aaggaacaga	cggtattcct	tgccgaagaa
301	gcaccggaca	acgttaaaac	aatgctccgc	agcaaaaggct	atttcagcag
351	caaggtcagc	ctgacggaaa	aagacggagc	ttatacgggtg	cacatcacac
401	cgggcccgcg	cacaaaaatc	gccaacgtcg	gcgtcgccat	cctcggcgac
451	atcctttcag	acggcaacct	cgccgaatac	taccgcaacg	cgctggaaaa
501	ctggcagcag	ccggtaggca	gcgatttcga	tcaggacagt	tgggaaaaaca
551	gcaaaaacttc	cgctctcggc	gcggtaacgc	gcaaaaggcta	cccgtttgcc
601	aagctcggca	acacccgggc	ggcgtcaac	cccgtataccg	ccaccgccga
651	tttgaacgtc	gtcgtggaca	gcggccgccc	cattgccttc	ggcgactttg
701	aaatcaccgg	cacacagcgt	taccccgaa	aaaccgtctc	cggcctggcg
751	cgcttccaac	cgggcacgcc	ctacgacctc	gacctgtctc	tcgacttcca
801	acaggcgctc	gaacaaaacg	ggcattatc	cggcgcgtcc	gtacaagccg
851	acttcgaccg	cctcccaagg	ggaccgcgtc	cccgtcaaaag	tcagcgtaaac
901	cgaggcctaaa	cgccacaaac	tcgaaaccgg	catccgcctc	gattcgggaat
951	acggtttggg	cggcaaaaatc	gcctacgact	attacaacct	cttcaacaaa
1001	ggctatatcg	gctcgggtcgt	ctgggatatg	gacaaatacg	aaaccacgct
1051	tgccgcgggc	atcagccagc	cgcgcaacta	tcggggcaac	tactggacaa
1101	gcaacgtttc	ctacaaccgt	tcgaccaccc	aaaacctcga	aaaacgcgcc
1151	ttctccggcg	gcattctgga	tgtgcgcgac	cgcgcgggca	tcgatgccag
1201	gctggggcg	gaattttctc	cagaaggccg	gaaaatcccc	ggctcggatg
1251	tcgatttggg	caacagccac	gccacgatgc	tgaccgcctc	ttggaacgc
1301	cagctgtc	acaacgtgct	gcaccccgaa	aacggccatt	acctcgacgg
1351	caaaatcggg	acgactttgg	gcacattcct	gtcctccacc	gcgtaattcc
1401	gcacctctgc	ccgcgcaggt	tattttctca	cgccccgaaa	caaaaaactc
1451	ggcacgttca	tcatacgcg	acaagcgggt	tacaccgttg	cacgcgacaa
1501	tgccgatgtc	ccctcggggc	tgatgttccg	cagcggcggc	gcgtcttccg
1551	tgcgcggtta	cgaacttga			

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

g286.pep

1	MQNTGTMMIK	PTALLLPALF	FFPHAYAPAA	DLSENKAAGF	ALFKSKSPDT
51	ESVKLKPFP	VRIDTQDSEI	KDMVEEHLPL	ITQQQEEVLD	KEQTGFLAEE
101	APDNVKTMLR	SKGYFSSKVS	LTEKDGYTV	HITPGPRTKI	ANVGVAIGLD
151	ILSDGNLAIEY	YRNALENWQQ	PVGSDFDQDS	WENSKTSVLG	AVTRKGYPLA
201	KLGNTRAAVN	PDTATADLNV	VVDSGRPIAF	GDFEITGTQR	YPEQTVSGLA
251	RFQPGTPYDL	DLLLDFQOAL	EQNGHYSAS	VQADFDRLP	GPRPRQSQRN
301	RGQTPQTRNR	HPFRFGIRFG	RQNRRLRLQP	LQQRLYRLGR	LGYGQIRNHA
351	CRRHQPAQQL	SGQLLDKQRF	LQPFDPKPR	KTRLLRRHLV	CARPRGRHRCQ
401	AGGGISRRRP	ENPRLGCRFG	QQPRHDADRL	LETPAAQORA	APRKRFLPRR

451 QNRDDFGHIP VLHRANPHLC PRRLEFLHARK QKTRHVHHTR TSGLHRCTRQ
 501 CRCPLGADV PRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq
 1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
 51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
 101 AAAACAAGGC GGCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACACC
 151 GAATCAGTCA AATTAAAACC CAAATTCCTC GTCCTCATCG ACACGCAGGA
 201 CAGTGAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCACGCAGC
 251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCGAAAGAA
 301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACGACG
 351 CAAAGTCAGC CTGACGAAA AAGACGGAGC TTATACGGTA CACATCACAC
 401 CGGGCCCCGC CACAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
 451 ATCCTTTTCA ACGGCAACCT CGCGCAATAC TACCGCAACG CGCTGGAAAA
 501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAACAA
 551 GCAAACTTTC CGTCCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
 601 AAGCTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
 651 TTTGAACGTC GTCGTGGACA GCGGCCGCCC CATCGCCTTC GGCAGCTTTG
 701 AAATCACCGG CACACAGCGT TACCCCGAAC AAATCGTCTC CGGCCTTGCG
 751 CGTTTTCCAG CCGGTATGCC GTACGACCTC GACCTGCTCG TCGACTTCCA
 801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
 851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
 901 GAGGTCAAAC GCCACAACT CGAAACCGGC ATCCGCCTCG ATTCCGGAATA
 951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
 1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAATAACGA AACACGCTT
 1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CGGGGCAACT ACTGGACAAG
 1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
 1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
 1201 CTGGGGGCGG AATTTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT
 1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
 1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC
 1351 AAAATCGGTA CGACTTTGGG CACATTCTTG TCCTCCACCG CGCTGATCCG
 1401 CACCTCTGCC CGTGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
 1451 GCACGTTTCA CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
 1501 GCGGACGTTT CTTCAAGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
 1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCC AACGGATCGG
 1601 TCCTGCCCGA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
 1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGATGCCCG
 1701 GCGCAATTTT AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
 1751 CTGCTTCAG CCCGCTGCG CCGTTTTCTT TCGACATCGC CTACGGGCAC
 1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep
 1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
 51 ESVKLPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFALAE
 101 APDNVKTMLR SKGYFSSKVS LTEKDGAITYV HITPGPRTKI ANVGVAILED
 151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
 201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
 251 RFQPGMPYDL DLLLDFQQAL EQNGHYSYGAS VQADFDRLQG DRVPVKVSVT
 301 EVKRHKLETG IRLDSEYGLG GKIAIDYNNL FNKGYSVSV WMDKYETTL
 351 AAGISQPRNY RGNWYTSNVS YNRSTTONLE KRAFSGGVWY VRDRAGIDAR
 401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
 451 KIGTTLGTFL SSTALIRTS RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
 501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
 551 FTRTLGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
 601 SDKKIRWHIS LGTRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKCLKPKFP					
	::					
g286	MQNTGTMMIKPTALLLPALFFFFPHAYAPAADLSENKAAGFALFKSKSPDTESVKCLKPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVL DKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVL DKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVA I LGDILSDGNLAEYYRNALENWQQPVGSDFDQDS					
g286	LTEKDGAYTVHITPGPRTKIANVGVA I LGDILSDGNLAEYYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTQA AVNPDTATADLNVVVDSGRPIAFGDFEITGTQR					
g286	WENSKTSVLGAVTRKGYPLAKLGNTRA AVNPDTATADLNVVVDSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDLDLLLD FQQALEQNGHYS GASVQADFDR L-QGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDLDLLLD FQQALEQNGHYS GASVQADFDR LPRGPRPRQSQRN					
	250	260	270	280	290	300
	300	310	320	330	340	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAYD YNLFNKG YIGSVVWMDKYETTLAAGISQPRN					
g286	RGQTPQTRNRHPPRFGIRFGRQNR LRLLOPLQORLYRLGR LGYQIRNHACRRHQPA AQL					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

a286.seq	1	51	101	151	201	251	301	351	401	451	501	551	601	651	701	751	801	851	901	951	1001	1051	1101	1151	1201	1251	1301
	ATGCACGACA	GGCTTTTATTT	AAAACAAGGC	GAATCAGTTA	TAGTGAATC	AGCAGGAAGA	GCACCGGACA	CAAAGTCAGC	CGGGCCCCGC	ATCCTTTTCAG	CTGGCAGCAG	GCAAAACTTC	AAGCTCGGCA	TTTGAACGTC	AAATTACCGG	CGCTTCCAAC	ACAGGCGCTC	ACTTCGACCG	GAGGTCAAAC	CGGTTTGGGC	GCTATATCGG	GCCGCCGGCA	CAACGTTTCC	TCTCCGGCGG	CTGGGGGCGG	CGATTTGGGC	AGCTGCTCAA
	CCCGTACCAT	TTCTTTCCGC	GGCGGGTTTC	AATTAACACC	AAGATATGG	AGTATTGGAC	ACGTTAAAC	CTGACGGAAA	CACCAAAATC	ACGGCAACCT	CCGGTAGGCA	CGTCCTCGGC	ACACCCGGGC	GTCGTGGACA	CAGCGAGCGT	CGGTTCCAAC	GAACAAACG	CCTCCAAGGC	GCCACAAGTC	GGCAAAATCG	TTCTGGTCGTC	TCAGCCAGCC	TACAACCGTT	CATCTGGTAT	AGTTTCTCGC	AACAGCCACG	CAACGTGCTG
	GATGATTAAA	ACGCATACGC	GCATATTGTTCA	CAAAATCCCC	TCGAAGAACA	AAGGAACAGA	AATGCTCCGC	AAGACGGAGC	GCCAACGTGC	CGCGAATAC	GTGATTTCGA	GCGGTAACGC	GGCCGTCAAC	GCGGCCGCC	TACCCCGAAC	CGGTTCCGTC	GGCATTATTC	GACCGCGTCC	CGAAACCGGC	CCTACGACTA	TGGGATATGG	GCGCAACTAT	CGACCACCCA	GTGCGCGACC	AGAAGGCCGG	CCACGATGCT	CATCCCGAAA
	CCGACCGCCC	GCCTGCCGCC	AAAACAAAAG	CTCCGCATCG	GCTGCCGCTC	CGGGCTTCCT	AGCAAAGGCT	TTATACGGTA	CGCTCGCCAT	TACCGCAACG	TACGGACAGT	GCAAAGCCTA	CCCGATACCG	CATCGCCTTC	AAATCGTCTC	GACCTGCTGC	CGGCGCGTCC	CCGTCAAAGT	ATCCGCCTCG	TTACAACCTC	ACGAATACGA	CGGGGCAACT	AAACCTCGAA	GCGCGGGCAT	AAAATCCCCG	AGCCGCCTCT	ACGGCCATTA
	TGCTCCTGCC	GACCTTTCCG	CCCCGACACC	ACACGCAGGA	ATACGCAGC	CGCCGAAGAA	ATTCAGCAG	CACATCACAC	CCTCGGCGAC	CGCTGGAAAA	TGGGAAAAACA	CCCGCTTGCC	CCACGCCCGA	GGCGACTTTG	CGGCTTGGCG	TCGGATTCCA	GTACAAGCCG	CAGCGTAACC	ATTCCGAATA	TTCAACAAGG	AACCAACGCT	ACTGGACAAG	AAACGCGCCT	CGATGCCAGG	GCTCGGATAT	TGGAACAGCC	CCTCGACGG

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1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCGA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTCCCGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTCCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

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This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

a286.pep

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1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAITV HITPGPRTKI ANVGVAAILGD
151 ILSDGNLAIE YRNALENWQQ PVGSDFDQDS WENKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLLDFQQA EQNGHYS GASVQADFDR LQDRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAIDYYNL FNKGYSV VMDMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL KRAFSGGIWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSDIDL NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGAFL SSTALIRTS RAGYFFTPEN KKLGTFLIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

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m286/a286 98.7% identity in 615 aa overlap

m286.pep	10	20	30	40	50	60
a286	10	20	30	40	50	60
m286.pep	70	80	90	100	110	120
a286	70	80	90	100	110	120
m286.pep	130	140	150	160	170	180
a286	130	140	150	160	170	180
m286.pep	190	200	210	220	230	240
a286	190	200	210	220	230	240
m286.pep	250	260	270	280	290	300
a286	250	260	270	280	290	300
m286.pep	310	320	330	340	350	360
a286	310	320	330	340	350	360
	370	380	390	400	410	420

670

m286.pep	RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG				
a286	RGNYWTSNVSYNRSTTQNLEKRAFSGGIWYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG				
	370	380	390	400	410
					420
	430	440	450	460	470
m286.pep	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLTGTFLSSTALIRTSARAGYFFTPEN				
a286	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLTGAFLSSTALIRTSARAGYFFTPEN				
	430	440	450	460	470
					480
	490	500	510	520	530
m286.pep	KKLGTFFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL				
a286	KKLGTFFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL				
	490	500	510	520	530
					540
	550	560	570	580	590
m286.pep	LVGSLLEYQLPFTRTSLGAVFHDMDGDAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH				
a286	LVGSLLEYQLPFTRTSLGAVFHDMDGDAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH				
	550	560	570	580	590
					600
	610				
m286.pep	SDKKIRWHISLGTRFX				
a286	SDKKIRWHISLGTRFX				
	610				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

```
g287.seq
1      atgtttaaac  gcagttgtgat  tgcaatggct  tgtatttttc  ccctttcagc
51     ctgtgggggg  ggcggtggcg  gatcgccgca  tgtcaagtcg  ggcgaacgcg
101    cgtcaaaaacc  ggcgcgcccc  gttgttgctg  aaaatgccgg  ggaaggggtg
151    ctgccgaaag  aaaagaaaga  tgaggaggca  gcgggcggtg  cgccgcaagc
201    cgatacgca  gacgcaaccg  ccggagaagg  cagccaagat  atggcggcag
251    tttcggcaga  aaatacaggc  aatggcggtg  cggaacaac  ggacaacccc
301    aaaaatgaag  acgcgggggc  gcaaaatgat  atgcgcgcaa  atgcgcgcga
351    atccgcaaat  caacgaggga  acaaccaacc  gcgcggttct  tcagattccg
401    cccccgcgtc  aaaccctgcc  cctgcgaatg  gcggtagcga  ttttggaagg
451    acgaacgtgg  gcaattctgt  tgtgattgac  ggaccgtcgc  aaaataatac
501    gttgacccac  tgtaaaggcg  attcttgtaa  tggtgataat  tttatgggat
551    aagaagcacc  gtcaaaatca  gaatttgaaa  aattaagtga  ttaagaaaaa
601    attaagcgat  ataaaaaaga  cgagcaacgg  gagaattttg  tcggtttggt
651    tgctgacagg  gtaaaaaagg  atggaactaa  caaatatatc  atcttctata
701    cggacaaacc  acctactcgt  tctgcacggt  cgaggaggct  gcttcgggcc
751    gagattccgc  tgattccgtg  caatcaggcc  gatacgtcga  ttgtggatgg
801    ggaagcggtc  agctcgaggc  ggcattccgg  caatatcttc  gcgccggaag
851    ggaattaccg  gtatctgact  tacggggcgg  aaaaattgcc  cggcggatcg
901    tatgccctcc  gtgtgcaagg  cgaaccggca  aaaggcgaaa  tgcttgttgg
951    cacggccgtg  tacaacggcg  aagtgtgcga  tttccatatg  gaaaaccggc
1001   gtccgtacc  gtcggaggc  aggtttgcgc  caaaagtcga  ttcggcgacc
1051   aaattctgtg  acggcattat  cgacagcgcg  gatgatttgc  atatgggtac
1101   gcaaaaattc  aaagccgcca  tcgatggaag  cggtttaag  gggacttgga
1151   cggaaaaatg  cggcgggat  gtttcgggaa  ggttttacgg  cccggccggc
1201   gaggaagtgg  cgggaaaaata  cagctatcgc  ccgacagatg  ctgaaaaggg
1251   cggattcagc  qtgtttgccg  qcaaaaaaga  tcgggattga
```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

1	<u>MFKRSVIAMA</u>	<u>CIFPLSACGG</u>	GGGGSPDVKS	ADTPSKPAAP	VVAENAGEGV
51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNP
101	KNEDAGAQND	MPQNAAESAN	QTGNNPAGS	SDSAPASNPA	PANGGSDFGR

```

151  TNVGNVSVID  GPSQNLTLTH  CKGDSNCGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR  ENFVGLVADR  VKKDGNTKYI  IFYTDKPPTR  SARSRRSLPA
251  EIPLIPVNQA  DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPGGS
301  YALRVQGEPA  KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVDDGIIDSG  DDLHMGTOKF  KAAIDGNFGK  GTWTENGSGD  VSGRFYGPAG
401  EEVAGKYSYR  PTDAEKGGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
  1  ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTTC  CCCTTTCAGC
 51  CTGCGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTCAAGTCG  GCGGACACGC
101  TGTCAAACAC  TGCCGCCCTT  GTTGTCTCTG  AAAAAGAGAC  AGAGGCAAAG
151  GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201  AGGCAGTCAA  GATATGGCGG  CGGTTTCGGA  AGAAAATACA  GGCAATGGCG
251  GTGCGGTAAC  AGCGGATAAT  CCCAAAATG   AAGACGAGGT  GGCACAAAAT
301  GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351  CCCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAAAATCAA  GCAACGGATG
401  CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451  GACGGAATGC  AGGGGGACGA  TCCGTCGGCA  GGCGGGCAAA  ATGCCGGCAA
501  TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551  CTTCAGATCC  CATCCCCGCG  TCAAACCCTG  CACCTGCGAA  TGGCGGTAGC
601  AATTTTGGA   GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651  GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701  ATTTCTTGGA  TGAAGAAGTA  CAGCTAAAAT  CAGAAATTGA  AAAATTAAGT
751  GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801  TGTCGGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851  TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901  GCACGGTCGA  GGCGGTGCGT  TCCGCGCGAG  ATGCCGCTGA  TTCCCGTCAA
951  TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTGAGC  CTGACGGGGC
1001  ATTCCGGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051  GGGGCGGAAA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAAGCGA
1101  ACCGGCAAAA  GGCGAAATGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151  TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGCAGG
1201  TTTGCCGCAA  AAGTCGATTT  CGGCAGCAAA  TCTGTGGACG  GCATTATCGA
1251  CAGCGCGCAT  GATTTCGATA  TGGGTACGCA  AAAATTCAAA  GCCGCCATCG
1301  ATGGAAACGG  CTTTAAGGGG  ACTTGGACGG  AAAATGGCAG  CGGGGATGTT
1351  TCCGGAAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGGCGG  GAAAATACAG
1401  CTATCGCCCG  ACAGATGCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGGCA
1451  AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
  1  MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSPKPAAP  VVSEKETEAK
 51  EDAPQAGSQ  QGAPSAQGSQ  DMAAVSEENT  GNGGAVTADN  PKNEDEVAQN
101  DMPQNAAGTD  SSTPNHTPDP  NMLAGNMENQ  ATDAGESSQP  ANQPDMANAA
151  DGMQGDPSA  GGQNAAGTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201  NFGRVDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251  DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIFYKPK  PTSFARFRRS
301  ARSRRSLPAE  MPLIPVNQAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351  GAEKLPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTGRG
401  FAAKVDFGSK  SVDGIIDSGD  DLHMGTOKF  AAIDGNFGFK  TWTENGSGDV
451  SGKFYGPAGE  EVAGKYSYRP  TDAEKGGFGV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEAK
          |||||
g287       MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKEKDEEA
          10      20      30      40      50      60

```

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT					
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQN	DMPQNA--					
		70	80	90	100	110	
m287.pep	110	120	130	140	150	160	169
g287	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAA	DGMQGD	DPSAGGQ	NAGNTA			
m287.pep	170	180	190	200	210	220	229
g287	AQGANQAGNNQAAGSSDPIFASNPA	PANGGSN	FGRVDLANGVLIDGPSQ	NITLTHCKGDS			
m287.pep	230	240	250	260	270	280	289
g287	CSGNNFLDEEVQLKSEFEKLS	DADKISNYKKD	GKNDKFVGLVADSVQ	MKGINQYIIFYKP			
m287.pep	290	300	310	320	330	340	349
g287	KPTSFAFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHS	GNIFAPEGNYRYLT					
m287.pep	350	360	370	380	390	400	409
g287	YGAEKLPGGSYALRVQGEPAKGEMLAGA	AVYNGEVLHFHTENGRPYPTRGRFAAKVD	FGS				
m287.pep	410	420	430	440	450	460	469
g287	KSV DGIIDSGDDLHMG	TQKFKA	AIDGNGFKGTWTENGSGD	VSGKFYGPAGEE	VAGKYSYR		
m287.pep	470	480	489				
g287	PTDAEKGGFGVFAGKKEQDX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

```
a287.seq
1  ATGTTTAAAC  GCAGTGTGAT  TGCAATGGCT  TGTATTGTTG  CCCTTTCAGC
51  CTGTGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTTAAGTCG  GCGGACACGC
101 TGTCCAAAACC  TGCCGCCCTT  GTTGTTACTG  AAGATGTCGG  GGAAGAGGTT
151 CTGCCGAAAG  AAAAGAAAGA  TGAGGAGGCG  GTGAGTGGTG  GCCCCGCAAGC
201 CGATACGCAG  GACGCAACCG  CCGGAAAGG  CGGTCAAGAT  ATGGCGGCAG
251 TTTCCGCGAGA  AAATACAGGC  AATGGCGGTG  CGGCAACAAC  GGATAATCCC
301 GAAAATAAAG  ACGAGGGACC  GCAAAATGAT  ATGCCGCAAA  ATGCCGCCGA
351 TACAGATAGT  TCGACACCGA  ATCACACCCC  TGCACCCGAA  ATGCCAACCA
401 GAGATATGGG  AAACCAAGCA  CCGGATCCCG  GGGAAATCGG  ACAACCGGCA
451 AACCAACCGG  ATATGGCAAA  TGCGGCGGAC  GGAATGCAGG  GGGACGATCC
501 GTCGGCAGGG  GAAAATGCCG  GCAATACGGC  AGATCAAGCT  GCAAATCAAG
551 CTGAAAACAA  TCAAGTCGGC  GGCTCTCAA  ATCCTGCCTC  TTCAACCAAT
601 CCTAACGCCA  CGAATGGCGG  CAGCGATTTT  GGAAGGATAA  ATGTAGCTAA
651 TGGCATCAAG  CTTGACAGCG  GTTCGGAAAA  TGTAACGTTG  ACACATTGTA
701 AAGACAAAGT  ATGCGATAGA  GATTTCTTAG  ATGAAGATGC  ACCACCTAAA
751 TCAGAATTTTG  AAAAATTAAG  TGATGAAGAA  AAAATTAATA  AATATAAAAA
```

```

801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTCTG GCGTTCTGCA CGGTCTGAGG GGTCTGCTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTCAGCCTG ACGGGGCATT CCGGCAATAT CTTCGCGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGTACAAC GGCGAAGTGC TGCATTTCCA TATGGAAAAC
1201 GGCCGTCCGT CCCCCTCCGG AGGCAGGTTT GCCGCAAAAG TCGATTTCCG
1251 CAGCAAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGGAAG ATGGCGGCGG GGATGTTTCC GGAAGGTTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGGAA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGGCGGATT CGGCGTGTTC GCCGGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

a287.pep

```

1 MFKRSVIAMA CIVALSAACG GGGSPDVKS ADTSLKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPOND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMQGGDDPSAG ENAGNTADQA ANQAENNVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDSGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRSLPAEM PLIPVNQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYLYTG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMFEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGDD LHMGTQKFKK VIDNGGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

```

m287/a287 77.2% identity in 501 aa overlap

```

              10      20      30      40
m287.pep      MFKRSVIAMACIFALSACGGGGGGSPDVKSADTSLKPAAPVSE-----KETE
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287           MFKRSVIAMACIVALSAACGGGGGGSPDVKSADTSLKPAAPVVTEDVGEEVLPKEKKDEEA
              10      20      30      40      50      60

              50      60      70      80      90      100     109
m287.pep      KEDAPQAGSQGQGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMPPQNAAGT
              |||| :| | :||:||||| |||||:|:|:|:|:| ||||| |||||
a287           VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADT
              70      80      90      100     110

              110     120     130     140     150     160     169
m287.pep      DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANADGMQGGDDPSAGGQNAAGNTA
              ||||| ||| :| | ||| ||||:||||| |||||:|:|:|:|:| |||||
a287           DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANADGMQGGDDPSAG-ENAGNTA
              120     130     140     150     160     170

              170     180     190     200     210     220     229
m287.pep      AQGANQAGNNQAAGSSDFIPASNPAANGGSNFGRVDLANGVLIDGPSQNTLTHCKGDS
              |:||||| ||||:|:|:| :||| :|||:||||:|:|:|:|:| :|:| :|:|:|
a287           DQAANQAENNVGGSQNPASSTNPATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV
              180     190     200     210     220     230

              230     240     250     260     270     280     289
m287.pep      CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIIFYKP
              |:|:|:|:| :||| ||||| :|:|:|:| :|:|:|:| :|:| :|:|:|
a287           CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKD
              240     250     260     270     280     290

              290     300     310     320     330     340
m287.pep      KP--TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRY
              | :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287           KSASSSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNRY
              300     310     320     330     340     350

```

674

	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDGIIDSGDDLHMGTQKFKAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVDGIIDSGDDLHMGTQKFKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVVFAGKKEQDX					
a287	YRPTDAEKGFGVVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1   atgcacaccg gacaggcggt aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgtctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgtttaccaa atgcgcgggt cgcccttacc gcaccttttc
201 acccttgccct gtgttgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgcccg ttaaccggca ttctaccctg
301 cggagcccg actttcctcc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggttat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacaggtt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccg tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPPL VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1   ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1   MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPPL VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF					
	: : : :					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADVFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

```

a288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTGCCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTGTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTGCTT GTGCTGCCAA AGCAGCCATC GCGGTTTTG CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC GCAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TAAAGCCGTC CAAGTCGCCG TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTGC GCAAGTCTTT AATGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

```

a288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHA
151 LFQAGFDKAV QVAVQYGFV ADFVACAQVF NA*

```

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADVFVACTQVF					
	: : : :					

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```
a288      PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFEVACAQVF
           130      140      150      160      170      180

m288.pep    DTX
           ::
a288      NAX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```
g290.seq
1  atggcaaaaa tgatgaaatg ggcggctgtt gcggcggtcg cggcggcagc
51  ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt cgcggtccaa cctggtatcg gtcggcgcg caggcttcggg
201 gcagattaaa aagctttatg tcaaactcgg gcaacagggt aaaaaggcgc
251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
351 tgcattgggc agcgcggaaa aaaaatataa gcgtcaggcg gcgttgtgga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 gccgccgcca aagccaatgt tgccgagttg aagcctttaa tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga tttgggctac acgcgcatta
551 ccgcgacgat ggacggcacg gtggtggcga ttccggtgga agaggggcag
601 actgtgaacg cggcgagtc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga ttttgtccga accggatacg
751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 tcggggcggc tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaatcgac ggtgtgaaaa atgtgttgct
951 tattccgctc ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacggc
1001 tgttgggtgc ggacggcaag gcagtggaac gcgaaatccg gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc gggttgaaag agggggacaa
1101 agtgggtcatc tccgaaataa ccgccgccga gcagcaggaa agcggcgaac
1151 gcgccctagg cggcccgcgc cgccgataa
```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```
g290.pep
1  MAKMMKWA AVAAVAWVG GWSYLPPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQQV KKGDLIAEIN STTQNTIDM
101 EKSLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARFV PNPDGKLTATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```
m290.seq (partial)
1  ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGGCGATTG GATTGCGGAA ATCAATTGCA
101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAACGTAT
151 CAGGCGAAGC TGGTGTGCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAGG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGGAAGAG GGGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GGCGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCTG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTCT TTTGTGCCGA
```

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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAAAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1 ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTL NTEKSKLETY
 51 QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTDTA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLI I PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

                                10      20      30
m290.pep                      VSVGAQASGQIKILYVKLGQVKKGDLIAE
                                |||||
g290      PQAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE
          30      40      50      60      70      80

                                40      50      60      70      80      90
m290.pep      INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRAALWKENATSKEDLESAQD
          |||:||||: |||||
g290      INSTTQNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKRAALWKDDATSKEDLESAQD
          90      100     110     120     130     140

                                100     110     120     130     140     150
m290.pep      AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
          |:|||||:|||||:|||||:|||||:|||||:|||||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPVEEGQTVNAAQST
          150     160     170     180     190     200

                                160     170     180     190     200     210
m290.pep      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          |||||
g290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          210     220     230     240     250     260

                                220     230     240     250     260     270
m290.pep      GGYNSSTDASNAVYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
          |||||
g290      GGYNSSTDASNAVYYARSFVPNPDGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
          270     280     290     300     310     320

                                280     290     300     310     320     330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
          |||||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
          330     340     350     360     370     380

m290.pep      PPRRX
          ||||
g290      PPRRX
          390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1   ATGGCAAAAA TGATGAAATG GGCGGCTGTT GCGGCGGTCG CGGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAC GGTCAAGCGC GCGGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTTATG TCAAACCTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTTGG AAAGCGACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TCGTTTGTG CCGAATCCGG ACGGCAAACG CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATTCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTTGGGTGC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1   MAKMMKWA AV AAVAAA AVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 EKSKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAANKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYARSFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```
m290.pep
10 20 30
VSVGAQASGQIKILYVKLGQOVKKGDLIAE
|||||
a290
30 40 50 60 70 80
PQAAYITETVRRGDISRTVSATGEISPSNLVS VSVGAQASGQIKKLYVKLGQOVKKGDLIAE

40 50 60 70 80 90
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||||
a290
90 100 110 120 130 140
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD

100 110 120 130 140 150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||
a290
150 160 170 180 190 200
ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST

160 170 180 190 200 210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||
a290
210 220 230 240 250 260
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS

220 230 240 250 260 270
```

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```

m290.pep      GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
                |||||
a290          GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
                270      280      290      300      310      320

                280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
                :|||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
                330      340      350      360      370      380

m290.pep      PPRRX
                ||||
a290          PPRRX
                390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggccttg gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgttctttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttgacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaattct atggtgtcag cccgaccgtg ccaaagcggtg gacggattgg
601 atgcgtaaa gcaaattccc ggtcggcgcc agcatctgcg acaatcccgt
651 cgcggaaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSVAAASLKAR
51  LEKTYSAQDL KVLVSVETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPOKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTCTTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGCGCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATCGGTAAG GCAAATTCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```

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751 CAACTGGAGG AAATCATCCG CAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSEF MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251  QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL					
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAESAVKAESAGKSPAASLKARLEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGKFPVGGISICDNPVAETTSLSGEQFGFNGTPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGKFPVGGISICDNPVAETTSLSGEQFGFNGTPTLRLPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPOKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1  ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101  TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151  TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTTGA GCGTCAGCGA
201  AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251  TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301  ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351  AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401  GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451  TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501  CAGCTTTATG ATGCCCATTT CCGGCCTGCA CCCCAGATGC GCGCGCAAGG
551  CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601  ATGCGTAAAG GCAAATTCCC GGTCCGGCGC AGCATCTGCG ACAATCCCGT
651  CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701  CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751  CAACTGGAGG AAATCATCCG CAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
51  LEKTYSAQDL KVLSVSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

m292/a292 100.0% identity in 260 aa overlap

              10      20      30      40      50      60
m292.pep    MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
              |||||
a292        MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
              10      20      30      40      50      60

              70      80      90     100     110     120
m292.pep    KVLSVSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              |||||
a292        KVLSVSETPVKGIYEVVVSQ RQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF
              70      80      90     100     110     120

              130     140     150     160     170     180
m292.pep    ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              |||||
a292        ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
              130     140     150     160     170     180

              190     200     210     220     230     240
m292.pep    ARKAQILWCQPDRAKAWTDWMRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
              |||||
a292        ARKAQILWCQPDRAKAWTDWMRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
              190     200     210     220     230     240

              250     260
m292.pep    RSQSGYSPMPQLEEIIRKNQX
              |||||
a292        RSQSGYSPMPQLEEIIRKNQX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
51  ggttcgggct gtcagaacat catcgaaccg ctttcctgcg gcgttacgac
101 gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151 tggcatcggg tgcggcggtt caagtcgaat cggcggacgc gtggcgtgaa
201 gccgttgaaa aaaccttata tggcgagggg ggcggaatgc agatgcaggc
251 gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301 ccgaggcggt gcgggaagcg gtatgcggac atcgggggcg atagtataac
351 aatccgtatc cgagttttcc ggttgagaca tcgtatgagt atttatgccg
401 tcgcgcacat catccacctg tattcgccca ccgcctttgt cggcggcggtg
451 ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgcgcg
501 cgaggcgcgg cgcgaaagtg aaaaggcaat gtcttaccgc gccgtcaggg
551 tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601 actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
1  MRITCAPMSL LSAAVWSVRA VRTSSNRFP A LRRYSAFRP TIFPKPAGTP
51  WHRVRRFKSN RRTRGVKPLK KPYLARGAEC RCRRAWTALS HNIAERARES
101 PRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFPAVG LLFARGTLES
201 TAAACP...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

m294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
151 TGGCATCGGG TCGGCGGCTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATAACGGAC GGGTGTGCGG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTGAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTTCGG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC GGTCGGTTGG
751 TCGAAATACA TACACGCCGT CGTCTTTACC CATATGcTGC TGATTGTCTT
801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep

```

1  MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRRYSAFQP TIFPKPADTP
51  WHRVRRFKSN RRMRGKPLK KPYRPRGGG RCRRRAWTALS HNIAERARES
101 PRRCGKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFIAIVVK MARSTLTVGW
251 SKYIHAVVFT HMLLIVFLAK AMFYISW*

```

g294/m294 92.3% identity in 196 aa overlap

g294.pep	10	20	30	40	50	60
m294	MRITCAPMSLLSAAVWSVRAVRTSSNRFFAALRRYSAFRPTIFPKPAGTPWHRVRRFKSN					
	10	20	30	40	50	60
g294.pep	70	80	90	100	110	120
m294	RRTRGVKPLKKPYLARGAECRCRRRAWTALSHNIAERARESPPRCGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
g294.pep	130	140	150	160	170	180
m294	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEVLSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
g294.pep	190	200				
m294	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFIAIVVK					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq

```

1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
151 TGGCATCGGG TCGGCGGCTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATAACGGAC GGGTGTGCGG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTGAGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTC CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTTCGG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

```


701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAFRP TIFPKPAGTP
 51 WHRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRTARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	VRTSSNRFPAAFRYSAFQPT	TIFPKPADTPWHRVRRFKSN			
a294	MRITCAPMSLLSAAVWSIRAV	VRTSSNRFPAAFRYSAFRPT	TIFPKPAGTPWHRVRRFKSN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGG	CRRAWTALSHNIAERARES	PRRCGKRYADIGGSDTIRI			
a294	RRTRGGKPLKKTYPRAEC	RCRRARTALSHNIAERARES	PRRYGKRYADIGGSDTIRI			
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVH	LYCAIAFVGGVFFEVLVLSVL	HTGRVSREARREVEKAMSYR			
a294	RVFRLEYRMSIYAVAHIVH	LYCAIAFVGGVFFEVLVLSVL	HTGRVSCEARREVEKAMSYR			
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMFVVGLLFASGIVMA	ANRYLSILGEPFATSFGTML	TLKILLAFSVLAHFAIAVVK			
a294	AVRVMFVVGLLFASGIVMA	ANRYLSILGEPFATSFGTML	TLKILLAFSVLAHFAIAVVK			
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVVF	THMLLIVFLAKAMFYISWX				
a294	MARSTLTVGWSKYIHTVV	FTHMLLIVFLAKAMFYISWX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcgga cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt tttccgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
 151 ctgcccggcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccga cactgcacg gatgccgcg ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 accgatcagg cggcggaact tcagataacc gttcagcgat tttccgcaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgccg gcattccttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcgggcg
 451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
 501 agcggcattg cgcacggga aacagaactt gcgcgggttc ccgtcccgtc
 551 ggggtcatct ggcgtatcag cagcggcgca tcgggaaaac gccgccgcaa
 601 ctgcgctatc aagggctggg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgcgggta acgggattcg gatcgggctt gccgaaacgc
 701 tcgtccctat gcgcccggta tgccggggca cttccggagc gttgtccaa
 751 ataacgcgt atccatatcg gcgcaagcag ccacaataca tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pep

```

1  MLGMARHDDGQ QGIAAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK
51  LPRQRFHVFR RHQVVFGLIAA HLHGCRAQFR QPRRIRLRLR QTARQSRGCG
101 TDQAADFQIT VQRFFRQPRI RQKQRHTRSP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLGRF PSRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```

1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCGGCCGG CCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTC TCTGTTCCGA CGGTATGATG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CGGCGGACTT TCAGATAACC GTTCAACGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCGG GCATTCCCTC
401 ATCAGGTTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAAGTCCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG CGCATCGGGA AACAGAACTT GCGCGGTTTC CCGCCCCGTC
551 GCGGTCATCT CGCTCATCAG CAGCGGCGCA TCGGGAAGAA GCCGCGCGAA
601 CTCGCGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGTCCCGAT GCGCCCGATA TGCCGGGGCA CTCCGGAGC GTTGTGTCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGCCC
801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC TGAACGGTTC
851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```

1  MLGMARHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK
51  LPRQRFHLFR RYDVVFGLIAA HLHGCRAQFR QPRRIRLCLR QTARQSRGGR
101 TDQAADFQIT VQRFFRQPRI RQKQRHTRAP AFPHQVGPDP GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL RIGKQNLGRF PRRGHLRHQ QRRIGKTPPQ
201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV XTQTAERQR NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQQRIAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPQRQFHLFR					
g295	MLGMARHDDQQGIAAILLPRRQOFFRLVFA PINARAAAHGNRPASDAFFKLPQRQFHVFR					
	10	20	30	40	50	60
m295.pep	RYDVVFGLIAAHLHGCRAQFRQPRRIRLCLRQTARQSRGGRTDQAADFQITVQRFFRQPRI					
g295	RHQVVFGLIAAHLHGCRAQFRQPRRIRLRLRQTARQSRGGCTDQAADFQITVQRFFRQPRI					
	70	80	90	100	110	120
m295.pep	RQKQRHTRAPAFPHQVGPDPGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLGRF					
g295	RQKQRHTRSPAFHLHQIGPDFGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLGRF					
	130	140	150	160	170	180
m295.pep	PPRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPN RAGNGIRIRLAETLVPMRPI					
g295	PSRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDRNGVYPN RAGNGIRMRLAETLVPMRPV					
	190	200	210	220	230	240
m295.pep	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTQTAERQRNQISX					
g295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVRTVRTAFRQRNQIS					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTCAAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTACAGGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTGCGGC AAAAAGTACC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GC CGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAAAAC GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCGGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFGLIAA HLHGCRAQFR QPRRIRLRLC QTARQSSGGR
101 TDQAADFQIT V*RRFRQPRI RQKQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
a295	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
a295	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
a295	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
a295	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
a295	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

```

51 GCTTGCCGTT TCGATTATTC TGGTGtcgGC GGCATACATT Gcttcgacag
101 aggggaccga ggcgctcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTtGGg ggcgcaacgg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCAGTGGC CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTCCG TTTGGAaaaa AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCTGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG CGCGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGCGGCGA
701 CAACCCATCA GGCCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGCGCGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TGC GCGGCGCG CGAGGTCATC GGTTTTGTCT GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACT TGCATTACGA GGC GCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

g297.pep

```

1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51 LSWGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSa REVQFFtDED GERNLVALEK KGGIWRRSAS
151 DADMKVLPtL RSVVVKTSAR GSLARAEPV EIRESLSGIF AGRFSLDGLK
201 EGDVAVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDYDEDGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTpVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPNVPVSV ALPTFELTQA
401 DKAAPAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

m297.seq

```

1 ATGGCTGTCT TCCCACtTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51 GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAAA TCTGCCGCCG
151 CTGTCTtGGG GCGGCAAGCG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCCTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTTAC CGACGAAGAC GGCAGCGCA
401 ATCTGGTCCG TTTGGAaaaG AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCTGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG CGCGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGCGGCGA
701 CAAGGCATCA GGCCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGCGCGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAAGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TGC GCGGCGCG CGAGGTCATC GGTTTTGTCT GTTCGACCGG
1101 GCGTTCGACC GGGCCGCACT TGCATTACGA GGC GCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

m297.pep

```

1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PQRVEQNLP
51 LSWGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSa REVQFFtDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPtL RSVVVKTSAR GSLARAEPV EIRESLSGIF AGRFSLDGLK

```

687

201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTTPVRA SADGVITFKG RGGYGNVAVM IRHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQORVEQNLPLPSWGGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQORVEQKLPPLSWGGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAVQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDDEGERNLVALEKKGGIWRSSASEADMKVLPPLRSVVVKTSARGSLARAEVVPV					
g297	REVQFFTDDEGERNLVALEKKGGIWRSSASDADMKVLPPLRSVVVKTSARGSLARAEVVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGRHQAFY					
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGRTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGNYYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGNYYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

```

1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA ACTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG TGTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCA GGCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGCGGCGCGC CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA
401 ATCTGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGTTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGCGCGCG GGTTCGCTGG CGCGGCGGGA AGTGCCCGTC GAAATTCGCG

```

```
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TCGCGGCGG CGAGGTCATC GGTTTTGTCT GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACT TGCATTACGA GCGCGCGCAT AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GCAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGC GCATACCGG TTACCGTGTC GCAATCGGAT TGA
```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```
a297.pep
1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PQRVEQKLPP
51 LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGG REVQFFTTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TLRSVVVKT SAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGT PVRASADGVITFKG RKGGYGNVAM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *
```

m297/a297 99.3% identity in 430 aa overlap

```
10 20 30 40 50 60
m297.pep MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV PQRVEQNLPPLSWGGSGVQT
a297 MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV PQRVEQKLPLPLSWGGSGVQT
10 20 30 40 50 60
70 80 90 100 110 120
m297.pep AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG
a297 AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG
70 80 90 100 110 120
130 140 150 160 170 180
m297.pep REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVVKT SARGSLARAEVPV
a297 REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLP TLRSVVVKT SARGSLARAEVPV
130 140 150 160 170 180
190 200 210 220 230 240
m297.pep EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQQVAAGDILAAEVVKGGTRHQAFY
a297 EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSLYFHGQQVAAGDILAAEVVKGGTRHQAFY
190 200 210 220 230 240
250 260 270 280 290 300
m297.pep YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
a297 YRSDKEGGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY
250 260 270 280 290 300
310 320 330 340 350 360
m297.pep AAPQGT PVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
a297 AAPQGT PVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
310 320 330 340 350 360
```

689

	370	380	390	400	410	420
m297.pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTGCGCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcgcgcgcac ggCTCAAGAC GGCGGTTCCG
251 CAGATATGCC GCCTGAAGCC GCCGCATCCG AAGCCGCCCC GCCGGCCGGC
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGAG ATTGCTGAT GCAGGGCGTT GCGCCTTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAGA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCCTGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTTACAT GAAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAAA ATCATCTCTA TTCCCACCGC
801 GCAAAACACT AGCGGCGGGA AAGGCCGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298.pep

```

1  MKNFLSLFAS ILMSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPPA
101 GTEWKQGTET AAVRSGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRILE AAHTRVQVV WLGIPLYMKV KLDGQMRYLD
251 KLLSEHLKKG IILIPTAOTL SGGKGRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCCG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTGCGCG ACTCGCTGAT GCAGGGCGTT GCGCCCTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACCCTGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATTT GAAAGGCAAA ATCATCTCTA TTCCCACCGC
801 GCACACCCTG AGCGGCGGGA AAGACCCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```

1  MKNFLSLFSS ILSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNPD WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVW WLGIPIYMKKA KLDGQMRYL
251 KLLSEHLKKG IILIPHTHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/g298 94.8% identity in 327 aa overlap

```

              10      20      30      40      50      60
m298.pep      MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRS
                |||
g298           MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRS
                |||
              10      20      30      40      50      60

              70      80      90     100     110     120
m298.pep      ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF
                |||
g298           ALSDGIKITFLSGETPPTAQDGGSDMPPEAAASEAAPAGGTEWKQGTAAAVRSGDKVF
                |||
              70      80      90     100     110     120

              130     140     150     160     170     180
m298.pep      FVGDSLMOGVAPFVQKSLKQQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV
                |||
g298           FAGDSLMOGVAPFVQKSLKQQYQYIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV
                |||
              130     140     150     160     170     180

              190     200     210     220     230     240
m298.pep      LAVFLGPNPDWDFPVGKLYLKFASDEWAQEYLKRVDRILEAAHTRVQVWVWLGIPYMKKA
                |||
g298           LAVFLGPNPDWDFPVGKRYLKFASDEWAQEYLKRVDRILEAAHTRVQVWVWLGIPYMKKV
                |||
              190     200     210     220     230     240

              250     260     270     280     290     300
m298.pep      KLDGQMRYLKLLSEHLKGGKIIILIPHTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA
                |||
g298           KLDGQMRYLKLLSEHLKGGKIIILIPHTHTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA
                |||
              250     260     270     280     290     300

              310     320
m298.pep      EGQKLLAAKIMEKIVFEPSTQPSSTQPX
                |||
g298           EGQKLLAEKIMEKIVFEPSTQPSSTQPX
                |||
              310     320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCCGCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCTTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACCTGGC
301 GAAACAGAAAT GGAAACAAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAA
501 GATTGAAGAA ACCCTGAAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GGCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCCTACAT GAAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

```



```

751  AAAGTCTTT  CGGAATATTT  GAAAGGCAAA  ATCATCCTGA  TTCCCACCGC
801  GCACACCCCTG AGCGGCGGGA  AAGACCGCTA  CACCGACTCC  GTCAACGTCA
851  ACGGCAAACC  CGTCCGCTAC  CGCAGCAAGG  ACGGCATACA  CTTTACCGCC
901  GAAGGACAAA  AACTGCTGGC  GGCAAAAATA  ATGGAAAAAA  TCGTTTTTGA
951  ACCAAGTACG  CAACCATCAA  GTACACAGCC  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1  MKNFLSLFAS  ILSALIAVW  FSQNPINAYW  QQTYHRNSPL  EPLAAYGWWR
51  SGAALQENAY  ALSDGIKAF  LSGETPPTAQD  GGSADMPSEA  AAPETAPQTG
101  ETEWKQNTA  AAVRTGDKVF  FAGDSLMOGV  APFVQKSLKQ  QYGIESVNL
151  KQSTGLSYPS  FFDWPKTIE  TLKKHPEISV  LAVFLGPNDP  WDFPVGKRYL
201  KFASDEWAQ  EYLKRVDRIL  AAHTHYVQVV  WLGI P YMKKA  KLDGQMR YLD
251  KLLSEYLGK  IILIPTAHTL  SGGKDRYTDS  VNVNGKPVRY  RSKDGIHFTA
301  EGQKLLAAKI  MEKIVFEPST  QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

```

              10      20      30      40      50      60
m298.pep      MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a298           MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
              10      20      30      40      50      60

              70      80      90      100     110     120
m298.pep      ALSDGIKAFSLSGETPPTAQDGGSDAMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a298           ALSDGIKAFSLSGETPPTAQDGGSDAMPSEAAAPETAPQTGETEWKQNTAEEAVRTGDKVF
              70      80      90      100     110     120

              130     140     150     160     170     180
m298.pep      FVGDSLMOGVAPFVQKSLKQYQYIESVNLKQSTGLSYPSFFDWPKTIEETLQKHPEISV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a298           FAGDSLMOGVAPFVQKSLKQYQYIESVNLKQSTGLSYPSFFDWPKTIEETLQKHPEISV
              130     140     150     160     170     180

              190     200     210     220     230     240
m298.pep      LAVFLGPNDPWDFPVGKLYLKFADEWAQEYLKRVDRILEAAHTRVQVWVWLGIPYMKKA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a298           LAVFLGPNDPWDFPVGKRYLKFADEWAQEYLKRVDRILEAAHTHYVQVWVWLGIPYMKKA
              190     200     210     220     230     240

              250     260     270     280     290     300
m298.pep      KLDGQMR YLDKLLSEHLKGKIIILIPTHTLSSGGKDRYTDSVNVNGKPVRYRSKDGIFHTA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a298           KLDGQMR YLDKLLSEYLGKIIILIPTAHTLSSGGKDRYTDSVNVNGKPVRYRSKDGIFHTA
              250     260     270     280     290     300

              310     320
m298.pep      EGQKLLAAKIMEKIVFEPSTQPSSTQPX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a298           EGQKLLAAKIMEKIVFEPSTQPSSTQPX
              310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1  ATGAACCCCA  AACACTTCAT  CGCATTITTC  GCCCTGTTCC  CCGCCACGCA
51  GGCAGAAGCC  CTGCCCCTCG  CCTCCGTCAG  CCCCACACCC  GTTACCGTTT
101  CCCCCTCCGC  CCCCTACACC  GATACAAACG  GGCTGCTGAC  CGACTACGGC
151  AACGCGCGCG  CCTCGCCTTG  GATGAAAAAA  CTCCGATCCG  TCGCACAAGG
201  CAGCGGCGAG  GCCTTCGCGA  TCCTGCAAAT  CGGCGACTCG  CATACCGCCG
251  GCGACTTCTT  TACCGACGCC  CTGCGCAAA  GCCTGCAAAA  AACATGGGGC
301  GACGGCGGCA  TAGGCTGGGT  TTACCCCGCC  AACGTCAAAG  GGCAGCGCAT
351  GCGGCGCGTC  CGTCACAGCG  GCAACTGGCA  AAGCTTCACC  AGCAGGAACA
401  ATACCGGAGA  TTTCCCGCTC  GCGGCGATCC  TCGCCCAAAC  CCGCAGCGGC
451  GCGGCGATGA  CCCTGACCGC  GTCTGACGGC  AAAACCGGCA  AACAGCGCGT

```

501	TTCCTGTTT	GCCAAACCGC	TGCTCGCCGA	ACAAACCCGT	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGCGCGCT	GCAGGTTACT	GGATACGGGG
601	GCGGCATCGC	CCCTGGCCAT	ACAGACCGAA	ATGCGTCGGG	ACATCGGCTT
651	CATCAACATC	GAAAATCCCG	CCGGCGGCAT	TACCGTTTCC	CGGATGGGCA
701	TCAACGCGCG	ACAATTAGCC	CAGTGGTCGA	AATGGCGCTC	CGACCGBTAT
751	AACGACCTTG	CCCAAAACGG	CGCCGATTTG	GTTATCTTTC	CCTACGGTAC
801	CAACGAGGCC	TCCAACAACA	ACATCGACAT	TGCGGATACC	GAAACAAAAT
851	GGCTGGATAC	CGTCCGCGAA	ATCCGCGACA	GCCTGCCCGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGCTCG	CGGTCCTCGG
951	CACGCGCCCC	TCTCTCTG	CGCAAGTCCA	ACAGATGACG	CGGCGCGTGC
1001	CCCGTCAGGG	GCAGACGATG	TTTTGGTCTT	GGCAAAACGC	AATGGGCGGC
1051	ATATGTCAGC	TGAAAAACTG	GCTCAACCGA	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTC	TCCGCCCAAG	GCTACCCGGG	CGGGCGGGAA	ATGCTTGGCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCGCCGCGC	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pcp

1	<u>MNPKHFI</u> <u>AF</u> <u>AE</u>	<u>ALFAATQ</u> <u>AE</u>	LPVASVSPDT	VTVSPSAPYT	DTNGLLLTDYG
51	NAAASVPMWK	LRSVAQGSSE	AFRIQLQIGS	HTAGDFFTTDA	LKRRLQKXTWG
101	DGGIGWVYPA	NVKGQORMAAV	RHSGNLQSFST	SRNNTGDFPL	GGIGALQDTSG
151	GGMTLTASDG	KTGKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	GGGQWQLTSG
201	AALPLAIQTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQPTGADL	VILSYGTNEA	FNNNIDIADT	EQKWLDTVRQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGTRP	VLLTEYVQQM	RRVARQGGOT	FWSWQNAMGG
351	ICSMKNWNLQ	GWAAKDGVHF	SAQGYVRAAE	MLADSLEBLV	FAAAIRO*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTCC	CCGCCACGCA
51	GGCAGAGGCC	CTACCTGTGC	CCTCCGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCCG	CCCCTACACC	GATACAACCG	GGCTGCTGAC	CGCATACGGC
151	AACGCCTCCG	CCTCGCTTTG	GATGAAAAAA	CTCAAACTCG	TGCGACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCTTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGAGTCTTT	TACCGACAGC	CTGCGCAAC	GCCTGCAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCGGTC	CGGCACAACG	GTAACCTGGC	AAGCTCAC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TGCGCCACAC	CGGCAGCGGC
451	GGCAGATGTA	CCCTGACCGC	ATCGGACCGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCTGTATT	GCCAAACCCC	TGCTTGCCGA	ACAAACCTCG	ACCGTCAACG
551	GCAACACCGT	TCCGCCAAC	CGCGCGCGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATG	GAAAACTCCG	CGCGCGGCAT	TACCGTTTCC	GGCATGGGTA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTCTG	AATGGCGTGC	CGACCGTATG
751	AACGACCTCG	CCCAAACCGG	CGCGGATTTG	GTTATCTCTT	CTACCGGCAC
801	CAACGAAGCT	TCAACAACA	ACATCGACAT	TGCCGACACC	GAACAAAAAT
851	GGTGTGATAC	CGTCCGCCAA	ATCCCGCACA	GCCTGCCTCG	CGCCGGCATC
901	CTCATCATCG	GCGCACCCGA	ATCCCTGAAA	AACACGCTCG	CGGTATGCGC
951	CACACGCCCC	TCCCGCTTGA	CCGAAGTCCA	ACAGATGCAG	CGCGCGCTCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	CATGGGCGGC
1051	ATATGTCAGCA	TGAAAAATAG	GCTCAACCGG	GGATGGGCGC	CCAAAGACGG
1101	CGTACACTTC	TCCCGCAAAG	GCTACCCGGC	CGCGGCGGAA	ATGCTCGCCG
1151	ACAGCTTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pap

1	<u>MNPKHLIAFS</u>	<u>ALFAATQAEA</u>	LPVASVSLDT	VTVSPSAPYT	DTNGLLTDYG
51	NASASPMWKK	LQSVAQGSSE	TFRILQIGDS	HTAGDFFTDS	LRKRLQKTWG
101	DGGIGWVYPA	NVKQGORMAAV	RHNGNWQSLT	SRNNTGDFPL	GGILATGSG
151	GSMTLTASDG	IASKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	GGGWQVLDTG
201	AALPLTIHTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQPTGADL	VILSYGCTEA	FNNNDIADT	RRKVLDTVRQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGTRP	VRLTEVQOMQ	EQVANRQQTG	FWSQWNAIMG
351	ICSMKNWNLQ	GWAAKDGVHF	SAGKYVRAAE	MLADSLEELV	RSAAIRO*

m299/g299 95.5% identity in 397 aa overlap

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDINGLLTDYGNASASPWMKK

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

i

1	ATGAACCCCA	AACACCTCAT	CGCATTTTCC	GCCCTATTCC	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTCT	CCTCAGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCCGC	CCCCTACACC	GATACAAACG	GGCTGCTGAC	CGACTACGGC
151	AACGCCTCCG	CCTCGCTTTG	GATGAAAAAG	CTCCAATTCC	TGCACAAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAAT	CGGCGACTCG	CATACCCGCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTACAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCGGTC	CGGCACAACG	GTAACCTGGCA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGACAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	CGCGCACTGC	CCCTGACCAT	ACACACGGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAATATCCG	CCGGCGGCAT	TACCGTTTCC	CGGATGGGCA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACCGG	CGCCGATCTA	GTCATCCTTG	CCTACGGTAG
801	CAACGAAGCC	TTCGGCGACA	ACATCGACAT	TGCCGATACC	GAACAGAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTACCTGC	CGCCGGCATC
901	CTCATCATCG	CGCGCGCCGA	ATCCCTGAAA	AACACGCTCG	CGGTATGCGG
951	CACACGCCCC	GTCCGCCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCATCG
1001	CCCCGTAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAACGCG	GATGGGCGGC
1051	GTTTGACAGCA	TGAAAAACTG	GCTCAACCCG	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTT	TCCGCGAAAG	GCTACCAACG	CTCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTD LKRLQKTWG
101  DGGIGWVYPA NVKGQRM AAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151  GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351  VCSMKNLNLH GWAAKDGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

m299.pep	10	20	30	40	50	60
	MNPKHLIAFSALFAATQAEALP	VASVSLDTVT	VSPSAPYTD	TNGLLTDY	GNASASPM	MKK
a299	MNPKHLIAFSALFAATQAEALP	VASVSLDTVT	VSPSAPYTD	TNGLLTDY	GNASASPM	MKK
	10	20	30	40	50	60
m299.pep	70	80	90	100	110	120
	LQSV AQSGE TFRILQIGDS	HTAGDFFTD	SLRKRLQKT	WGDGGIGW	VYPANVKG	QRM AAV
a299	LQSV AQSGE TFRILQIGDS	HTAGDFFTD	SLRKRLQKT	WGDGGIGW	VYPANVKG	QRM AAV
	70	80	90	100	110	120
m299.pep	130	140	150	160	170	180
	RHNGNWQSLTSRNNTGDF	PLGGILAHT	GSGGSMTLT	ASDGIASK	QRVSLFA	KPLLAEQTL
a299	RHNGNWQSLTSRNNTGDF	PLGGILAHT	GSGGSMTLT	ASDGIASK	QRVSLFA	KPLLAEQTL
	130	140	150	160	170	180
m299.pep	190	200	210	220	230	240
	TVNGNTVSANGGGWQVLD	TGAALPLTI	HTEMPWDI	GFINIEN	PAGGITVS	AMGINGAQLT
a299	TVNGNTVSANGGGWQVLD	TGAALPLTI	HTEMPWDI	GFINIEN	PAGGITVS	AMGINGAQLT
	190	200	210	220	230	240
m299.pep	250	260	270	280	290	300
	QWSKWRADRMNDLAQTG	ADLVILSYGT	NEAFNNN	IDIADTEQ	KWLDTVRQ	IRDSLPAAGI
a299	QWSKWRADRMNDLAQTG	ADLVILAYGT	NEAFGDNI	DIADTEQ	KWLDTVRQ	IRDSLPAAGI
	250	260	270	280	290	300
m299.pep	310	320	330	340	350	360
	LIIGAPESLKNTLGVCGR	PVRLTEVQQ	MQRVARQ	QTMFWSW	QNAMGGIC	SMKNWLNQ
a299	LIIGAPESLKNTLGVCGR	PVRLTEVQQ	MQRRIARQ	QTMFWSW	QNAMGGVCS	MKNWLNH
	310	320	330	340	350	360
m299.pep	370	380	390			
	GWAAKDGVHFS	SAKGYRRAE	MLADSLEEL	VRSAAIRQ		
a299	GWAAKDGVHFS	SAKGYQSAE	MLADSLEEL	VRSAAIRQ		
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
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351  GGGGATTGCG  GAAAAATCGG  GCTTGATTTC  CGCATTAATG  CGCTTATTGC
401  TCACAAAATC  CCCACGCAAA  CTCACTACTT  TTATGGTTGT  TTTTACAGGG
451  ATTTTATCCA  ATACGGCTTC  TGAATTGGGC  TATGTCGTCC  TAATCCCTTT
501  GTCCGCCGTC  ATCTTTCATT  CGCTCGGCCG  CCATCCGCTT  GCCGGTTTGG
551  CTGCGGCTTT  CGCCGGCGTT  TCGGGCGGTT  ATTCGGCCAA  TCTGTTCTTA
601  GGCACAATCG  ATCCGCTCTT  GGCAGGCATC  ACCCAACAGG  CGGCGCAAAT
651  CATCCATCCC  GACTACGTCG  TAGGCCCTGA  AGCCAACCTG  TTTTTTATGG
701  CAGCCAGTAC  GTTTGTGATT  GCTTTGATTG  GTTATTTTGT  TACTGAAAAA
751  ATCGTCGAAC  CGCAATTGGG  CCCTTATCAA  TCAGATTTGT  CACAAGAAGA
801  AAAAGACATT  CGGCATTCCA  ATGAAATCAC  GCCTTTGGAA  TATAAAGGAT
851  TAATTTGGGC  AGGCGTGGTG  TTTGTTGCCT  TATCCGCCCT  ATTGGCTTGG
901  AGCATCGTCC  CTGCCGACGG  TATTTTTCGT  CATCCTGAAA  CAGGATTGGT
951  TGCCGGTTCG  CCGTTTTTAA  AATCGATTGT  TGTTTTTATT  TTCTTGTGT
1001  TTGCGCTGCC  GGGCATTGTT  TATGGCCGGA  TAACCCGAAG  TTTGCGCGGC
1051  GAACGGGAAG  TCGTTAATGC  GATGGCCGAA  TCGATGAGTA  CTTTGGGACT
1101  TTATTTGGTC  ATCATCTTTT  TTGCCGCACA  GTTGTGCGCA  TTTTAAATT
1151  GGACGAATAT  TGGGCAATAT  ATTGCCGTTA  AAGGGGCGGT  GTTCTTAAAA
1201  GAAGTCGGCT  TGGGCGGCAG  TGTGTTGTTT  ATCGGTTTTA  TTTTAATTG
1251  TGCTTTTATC  AATCTGATGA  TAGGCTCCGC  CTCCGCGCAA  TGGGCGGTAA
1301  CTGCGCCGAT  TTTCTGCCCT  ATGCTGATGT  TGGCCGGCTA  CGCGCCCCAA
1351  GTCATTCAAG  CCGCTTACCG  CATCGGTGAT  TCCGTTACCA  ATATTATTAC
1401  GCCGATGATG  AGTTATTTTC  GGCTGATTAT  GGCGACGGTA  ATCAAATACA
1451  AAAAAGATGC  GGGCGTAGGC  ACGCTGATT  CTATGATGTT  GCCGTATTCC
1501  GCTTTCTTCT  TAATTGCATG  GATCGCCTTA  TTCTGCATTT  GGGTATTGT
1551  TTTGGTCTG  CCCGTCGGTC  CCGGCACACC  CACATTCTAT  CCGGTGCCCT
1601  AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1  MHSIYFFKEK  QMSQTDARRS  GRFLRTVEWL  GNMLPHPVTL  FIIFIVLLLI
51  ASAVGAYFGL  SVPDPRPVGA  KGRADDGLIH  VVSLLDADGL  IKILTHTVKN
101  FTGFAPLGTV  LVSLLGVGIA  EKSGGLISALM  RLLLTGKSPRK  LTFMVVFTG
151  ILSNTASELG  YVVLIPLSAV  IFHSLGRHPL  AGLAAAFAGV  SGGYSANLFL
201  GTIDPLLAGI  TQQAQIIHP  DYVVGPEANW  FFMAASTFVI  ALIGYFVTEK
251  IVEPQLGPYQ  SDLSQEEKDI  RHSNEITPLE  YKGLIWAGVV  FVALSALLAW
301  SIVPADGILR  HPETGLVAGS  PFLKSIVVFI  FLLFALPGIV  YGRITRSLRG
351  EREVVNAMAE  SMSTLGLYLV  IIFFAAQFVA  FFNWTNIGQY  IAVKGAVFLK
401  EVGLGGSVLF  IGFI LICA FI  NLMIGSASAQ  WAVTAPIFVP  MLMLAGYAPQ
451  VIQAAAYRIGD  SVTNII TPMM  SYFGLIMATV  IKYKKGAVG  TLISMMLPYS
501  AFFLIAWIAL  FCIWVFLGL  PVGPGTPTFY  PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1  ATGCACTCAA  TATATTTTTT  TAAGGAGAAG  CAGATGAGTC  AAACCGATAC
51  GCAACGGGAC  GGACGATTTT  TACGCACAGT  CGAATGGCTG  GGCAATATGT
101  TGCCGCATCC  GGTTACGCTT  TTTATTATTT  TCATTGTGTT  ATTGCTGATT
151  GCCTCTGCCG  TCGGTGCGTA  TTTCCGACTA  TCCGTCCCCG  ATCCGCGCCC
201  TGTTGGTGCG  AAAGGACGTG  CCGATGACGG  TTTGATTTAC  ATTGTCAGCC
251  TGCTCAATGC  CGACGGTTTT  ATCAAAATCC  TGACGCATAC  CGTTAAAAAT
301  TTCACCGGTT  TCGCGCCGTT  GGAACGGTG  TTGGTTTCTT  TATTGGGCGT
351  GGGGATTGCG  GAAAAATCGG  GCTTGATTTC  CGCATTAATG  CGCTTATTGC
401  TCACAAAATC  GCCACGCAAA  CTCACTACTT  TTATGGTTGT  TTTTACAGGG
451  ATTTTATCTA  ATACCGCTTC  TGAATTGGGC  TATGTCGTCC  TAATCCCTTT
501  GTCCGCCATC  ATCTTTCATT  CCCTCGGCCG  CCATCCGCTT  GCCGGTCTGG
551  CTGCGGCTTT  CGCCGGCGTT  TCGGGCGGTT  ATTCGGCCAA  TCTGTTCTTA
601  AGCACAATCG  ATCCGCTCTT  GGCATGCATC  ACCCATCAGG  CGGCGGTCGT
651  AGGCCCTGAA  GCCAACTGGT  TTTTATGGT  AGCCAGTACG  TTTGTGATTG
701  CTTTGATTGG  TTATTTTGT  ACTGAAAAAA  TCGTCGAACC  GCAATTGGGC
751  CCTTATCAAT  CAGATTTGTC  ACAAGAAGAA  AAAGACATTC  GGCATTCCAA
801  TGAAATCACG  CCTTTGGAAT  ATAAAGGATT  AATTTGGGCT  GGCGTGGTGT
851  TTGTTGCCTT  ATCCGCCCTA  TTGGCTTGGA  GCATCGTCCC  TGCCGACGGT
901  ATTTTTCGTC  ATCTGAAAC  AGGATTGGTT  TCCGTTTCGC  CGTTTTTAAA
951  ATCGATTGTT  GTTTTTATTT  TCTTGTGTT  TGCATGyCG  GGCmTTGTTT
1001  ATGGmCGGGT  AACCCGAAGT  TTGCGCGGCG  AACAGGAAGT  CGTTAATGCG

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1051 ATGCCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kcATCTTTTT
1101 TGCCGCACAG TTTGTGCGCAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTAA AGGGGCGACG TTCTTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TGCGCCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCGG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GGCCTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1  MHSIYFFKEK QMSQTDQD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDPRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVVFALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXXIFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIFILIC AFINLMIGSA SAQWAVTAPI FVPMLLAGY APEVIQAAAYR
451 IGDVSTNIIT PMSYFGLIM ATVIKYKKA GVGTLISMML PYSAFFLIAW
501 IALFCIWVVFV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

m302.pep	10	20	30	40	50	60
	MHSIYFFKEKQMSQTDQDGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
m302.pep	70	80	90	100	110	120
	SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
g302	SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	70	80	90	100	110	120
m302.pep	130	140	150	160	170	180
	EKSLISALMRLLLTSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
g302	EKSLISALMRLLLTSPRKLTTFMVFTGILSNTASELGYVVLIPLSAIIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	190	200	210	220	230	
	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQQAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	240	250	260	270	280	290
	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
g302	ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVFALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFI FLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFI FLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGILICAFI
          |||||:|||||:|||||:|||||:|||||
g302      SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||
g302      NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKGAGVGTLSMMLPYSAFFLIWIALFCIWVFLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||
g302      IKYKKGAGVGTLSMMLPYSAFFLIWIALFCIWVFLGLPVGPGTPTFFYPVPX
          490      500      510      520      530

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1   ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGACTA TCCGTCCCGG ATCCGCGCCC
201 TGTGTGTCG AAAGGACGTG CCGATGACGG TTTGATTACG GTTGTCAGCC
251 TGCTCGATGC TGACGTTTGG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCGGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGCG TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTTCGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 TAGCCAGTAC GTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGCGGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTTGTTT ATCGGTTTTA TTTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTGTG
1551 TTTGGGCCCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1   MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHVPTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVVFTE

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKGAVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

```

              10      20      30      40      50      60
m302.pep      MHSIYFFKEKQMSQTDQDGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAVGAYFGL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           MHSIYFFKEKQMSQTDQDGRFLRTVEWLGNMPLPHPVTLFIIIFIVLLLIASAAGAYFGL
              10      20      30      40      50      60

              70      80      90     100     110     120
m302.pep      SVPDPRPVGAKGRADDGLIYIVSLLNADGFIKILHTVKNFTGFAPLGTVLVSLGVGIA
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           SVPDPRPVGAKGRADDGLIHVVSLLDADGLIKILHTVKNFTGFAPLGTVLVSLGVGIA
              70      80      90     100     110     120

              130     140     150     160     170     180
m302.pep      EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIIFHSLGRHPL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           EKSGLISALMRLLLTKSPRKLTTFMVVFTGILSNTASELGYVVLIPLSAIIIFHSLGRHPL
              130     140     150     160     170     180

              190     200     210           220           230
m302.pep      AGLAAAFAGVSGGYSANLFLSTIDPLLAGITQAA-----VVGPEANWFFMVASTFVI
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMVASTFVI
              190     200     210     220     230     240

              240     250     260     270     280     290
m302.pep      ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVV FVALSALLAW
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           ALIGYFVTEKIVEPQLGPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVV FVALSALLAW
              250     260     270     280     290     300

              300     310     320     330     340     350
m302.pep      SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALPGIVYGRVTRSLRGEQEVVNAMAE
              310     320     330     340     350     360

              360     370     380     390     400     410
m302.pep      SMSTLXLXLXXIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGFILICAFI
              370     380     390     400     410     420

              420     430     440     450     460     470
m302.pep      NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIITPMMSYFGLIMATV
              430     440     450     460     470     480

              480     490     500     510     520
m302.pep      IKYKKGAVGTLISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a302           IKYKKGAVGTLISMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFYPAPX
              490     500     510     520     530

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

g305.seq

```

1  ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTTTGG GGTAGTGTTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GTGTTGCCCA AGTGTGTTGCA CTGGTCCCG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GACGGAAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TTCCGATGAT GGTGTCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCCT GGTGTTGGTAG
701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
801 GGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLIAIAF IPAAVMGLLF
101 DKQIKLEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1  AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTTTGG GGTAGTGTTT GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCawACAAA TCAAAGAGyA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTtTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTCCCG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGCTG TGCCGATGAT GGTGCGCGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCCTA GGCTTGGTAG
701 CGGTAAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLIAIAF IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

```

          10      20      30      40      50      60
g305.pep  MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
          |||
m305       MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
          10      20      30      40      50      60

```

700

	70	80	90	100	110	120
g305.pep	EYRQRFSNVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
m305	EYRQRFSNVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEYLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGGMLWGI					
m305	XGFXILWVEKRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1   ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTGGG GGTAGTGTTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTGTTTC
301 GGCAAACAAA TCAAAGAGTA TCTGTTTAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGTC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCCG TTCCGATGAT GGTTGCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTCCTA GGCTTGGTGG
701 CCGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1   MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAIAE IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK RQSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFSNVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEYLFNPLSVAVMLVL					
a305	EYRQRFSNVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRSRAEPK	ADVDALRPIDALMIGVAQVFALVP	PGTSRSGSTIMGGM	LWGI		
a305	GGFFILWVEKRSRAEPK	IVDVALRPIDALMIGVAQVFALVP	PGTSRSGSTIMGGM	LWGI		
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVL	KHYRFFTLHDVGLILIGFIAAFVSG	LVAVKALLR			
a305	ERKTATEFSFFLAVPMMVAATAYDVL	KHYRFFTLHDVGLILIGFVAAFVSG	LVAVKALLR			
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSG	WISWEX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

g306.seq

```

1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGTCTGT  CCGGTTTCTT
51  CTTCCGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAAGTTG  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGCGCG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCC
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

g306.pep

```

1  MFMNKFSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKALTE  EEREQTVREK  AQKKAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

m306.seq (partial)

```

1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCAGmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAwCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGATGTC  GGAAAAwGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTAAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
 701 GCGGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)
 1 ..GLFFGLILAT VIIAGILFYLNQSGQNAFKI PASSKQPAET EILKPNQXK
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
 101 EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
 151 SKEEKKAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
 251 MR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

m306.pep	10	20	30	40
	GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX			
g306	MFMNKFSQSGKGLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK			
	10	20	30	40
	50	60	70	80
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
g306	NQPKEDIQPEPADQNALSEPDVAKEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKKAVKPSKETEKKASKEEKKAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGGGSQRIICKWARMNPNGARKGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPKWSAIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq
 1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT
 51 CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC
 101 TGAACCAGAG CGGTCAAAT GCGTCAAAA TCCCGGTTC GTCGAAGCAG
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAAG GCGGACGAGC CGGAGCGGGA
 351 AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
 451 AAACAAGCGG TAAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAGA
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```

601 GAAGTGCAGA AAATGAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTCCGGTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGGT
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KGLSGFFFGL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD GQAVRKKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKASKEEK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

m306.pep          10      20      30      40
                    GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPK
                    |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a306              10      20      30      40      50      60
MFMNKFSQSGKGLSGFFFGLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK

m306.pep          50      60      70      80      90     100
NQXKEDIQXPADQNALSEPDAATEAEQSDAEAXADKQPVADKADEVEEKAGEPEREEDP
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a306              70      80      90     100     110     120
NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD

m306.pep          110     120     130     140     150     160
GQAVRKKALTEEREQTVREKAQKKDAETVKKQAVKPSKETEKASKEEKKAKEKVAPKP
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a306              130     140     150     160     170     180
GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKASKEEKKAKEKVAPKP

m306.pep          170     180     190     200     210     220
TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a306              190     200     210     220     230     240
TPEQILNSGSIEKARSAAAKEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY

m306.pep          230     240     250
LPRWSVIRRDIKFTGCKAAICLPMRX
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a306              250     260
LPRWSVIRRDIKFTGCKAAICLPMRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1 atgaaaacct tcttcaaaac ctttcgacc gcgtcactcg cgctcatcct
51 cgagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gccggaatct ggcatggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaacctt atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gaccgcgtcca acttcgcacg cgccttggtg atgctgaacg aactggggtg
501 gatcaaatc aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcggaata cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```

```

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggctta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgcagc caaataa

```

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

```

g307.pep
  1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSDNG AAKKEIVFGT
 51 TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFQ
101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLSLEEV KDGSTVSAPN
151 DPSNFARALV MLNELGWIKL KGINPLTAS KADIAENLKN IKIVELEAAQ
201 LPRSRADVDF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS
251 QWLKDVTEAY NSDAFKAYAH KRFEQYKYP A WNEGA AK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

```

m307.seq (partial)
  1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG
101 AAGGCGCAGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

```

m307.pep (partial)
  1 ..QWLKDVTEAY NSDAFKAYAH KRFEQYKSPA A WNEGA AK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

```

m307/g307

m307.pep                                10      20      30
                                QWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
g307      SGMKLTEALFQEPSFAYVNWSAVKTDKDSQWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
                                230      240      250      260      270      280

m307.pep      39
      A WNEGA AKX
g307      A WNEGA AKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

```

a307.seq
  1 ATGAAAACCT TCTTCAAAAC CCTTTCCGCC GCCGCACTCG CGCTCATCCT
 51 CGCCGCCGTC GCGGTCAAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
101 CCGCCGCCGA CAACGGCGCG GCGAAAAAAG NAATCGTCTT CCGCACGACC
151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
201 GAAAAAAGGC TACACCGTCA AACTGGTCTG GTTTACCGAC TATGTGCGCC
251 CGAATCTGGC ATTGGCTGAG GGCGAGTNGG ACATCAACGT CTTCCAACAC
301 AAACCTATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATCACC GA
351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCCG GGCAAGCTGA
401 AATCGCTGGA AGAAGTCAA GACGGCAGCA CCGTATCCGC GCCCAACGAC
451 CCGTCCAAC TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
501 CAACTCAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
551 CCGAAAACCT GAAAAACATC AAAATCGTCT AGCTTGAAGC CGCGCAACTG
601 CCGCGTAGCC GCGCCGACGT GGATTTTGN CCGTCAACG GCAANTACGC
651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
701 TTGCCTATGT CAACTGGTCT GCGTCAAAA CCGCCGACAA AGACAGCCAA
751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
851 GCGCAGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

```

a307.pep
  1 MKTFFKTLA AALALILAAC GGQKDSAPAA SASAADNGA AKKXIVFGTT

```

705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDEFKE  HNLDITEVFQ  VPTAPLGLYP  GKLKSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKNI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEQYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAKX
          |||||
a307      AWNEGAAKX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101  TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151  GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAAC
201  TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251  AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301  TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351  CCGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTCTG  TCGATGCCGA
401  CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451  GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501  AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551  TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCGA
601  ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651  CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVIFYRI  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RRMVVRRLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101  LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTLRA
151  ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPO
201  TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101  TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151  GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGAAC
201  TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251  AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301  TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351  CCGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCCGA
401  CGCTTGCCCT  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGcT  GACGCGTGCG
451  GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501  AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAA
551  TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601  ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGcT  TGTCGCTGTT
651  CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIIA  GLPLQAVLWE  RMMVRRLLII
51 GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMKR  XTEGGVVFPP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

m308.pep	10	20	30	40	50	60
	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
	10	20	30	40	50	60
m308.pep	70	80	90	100	110	120
	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308.pep	130	140	150	160	170	180
	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
	130	140	150	160	170	180
m308.pep	190	200	210	220	230	
	XTEGGVVFPPVVPAMYRKPOADDIVAHSVVAHLSLFGIDTPDSAEOQGM					
g308	VTEGGVVFPPVVPAMYRKPOADDIVAHSIAHTLSLFGIDTPDLAEOQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIIA  GLPLQAVLWE  RMMVRRLLII
51 GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMXR  VTEGGVVFPP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  AD*

```


m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRLIIIGISGASGFQY					
a308	MLNRIFYRILGVADNLYPYLSDFCFFTTIIAGLPLQAVLWERRMMVRLIIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFVHPIGNIGACIASGTF					
a308	GVKALXLLRAQDIETHLVVSKGAEMARSETXYARDXVYALADXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFNDLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
a308	KTDGMLVAPCSMRTLASVVHGFNDLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKPTADDIVAHSVAHLSLFGIDTPDSA EWQGM A					
a308	VTEMGGVVFPVPAMYRKPTADDIVAHSVAHLSLFGIDTPDSA EWQGM ADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTTCGCCGT
101 TGCAGCGCGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GGCCTGAAGG CTTTGGAAC T
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGCGCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCGT CGATGTACCG CAAGCCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTTIIA GLPLQAVLWE RRMVRLII
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKQP
201 TADDIVAHSI AHTLSLFGID TPDLA EWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTTCGCCGT
101 TGCAGCGCGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GGCCTGAAGG CTTTGGAAC T
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGTGCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCCGT CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTTIIA GLPLQAVLWE RRMVRLII

```

```

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSV AHALSFGID TPDSAEOQGM AD*

```

m308-1/g308-1 97.0% identity in 232 aa overlap

```

              10      20      30      40      50      60
m308-1.pep  MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              |||||
g308-1      MLNRVFYRILGVADNLYPCLSDFCFFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              10      20      30      40      50      60

              70      80      90      100     110     120
m308-1.pep  GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF
              |||||
g308-1      GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADVFHPIGNIGACIASGTF
              70      80      90      100     110     120

              130     140     150     160     170     180
m308-1.pep  KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVKERRRLVLMVRETPLNLAHLDNMKR
              |||||
g308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVKERRRLVLMVRETPLNLAHLDNMKR
              130     140     150     160     170     180

              190     200     210     220     230
m308-1.pep  VTEMGGVVFPVPAMYRKPOADDIVAHVAHALSLFGIDTPDSAEOQGMADX
              |||||
g308-1      VTEMGGVVFPVPAMYRKPOADDIVAHSLAHTLSLFGIDTPDLAEOQGMADX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

```

1  ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGTATTTA TCGGATTTCT GTTTTTCAC TATAATAGCC GGTGTTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GGCCTGAAGG CTTGGANCT
201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
301 TTGGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCCT GGTCTGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCGTTCCTG CGATGTACCG CAAACCGCAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

```

1  MLNRIFYRIL GVADNLYPYL SDFCFFTIIA GLPLQAVLWE RRMVRRLLI
51  GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSV AHALSFGID TPDSAEOQGM AD*

```

a308-1/m308-1 96.1% identity in 232 aa overlap

```

              10      20      30      40      50      60
a308-1      MLNRIFYRILGVADNLYPYLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              |||||
m308-1      MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              10      20      30      40      50      60

              70      80      90      100     110     120
a308-1      GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF
              |||||
m308-1      GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF
              70      80      90      100     110     120

              130     140     150     160     170     180
a308-1      KTDGMLVAPCSMRTLASVHGFNDNLTRAADVVKERRRLVLMVRETPLNLAHLDNMKR
              |||||

```

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNL LTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPVPVAMYRK PQ TADDIVAH SVAHALSLFGIDTPDSA EWQGMADX
              |||||
m308-1      VTEMGGVVFPVPVAMYRK PQ TADDIVAH SVAHALSLFGIDTPDSA EWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1   atgttcagtt tcggtcgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgcct gttgcggcac ttgcgtgccg gcgcgctttg ggggtgtttg
101 gtttggaaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaaacagtc agggcgggcg gtaaaacggt
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tgggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tctgtgttga aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgccg taccgcgatt
701 tgtcgccttt gggcgcgga gggcgggaaa aggcggatgg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgcga caggctttgg
851 gcatacgcaa ccaactaccg caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtta cggttgacgc gctcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggttccc acctgatgaa agaatcgcctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg caccgcccgt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcggcgcgcg cgaaagtccg
1251 cgaagccctg ccgcctgcat ttttggcgga aaataccgtg cgcgtggcgg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaaggcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILIE TV RAGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLE TL LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVHLLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLLLEGGN SRLKWAVVEN GTFATVGSAP YRDLSP LGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNH YR HPEEHGSDRW
301 FNALGSR RFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLN RP AGKRYPFPTT TGNVAVSGMM DAVCGS IMMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGTG CGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCATTTAAG TGGCCCAATG ATTTGGTTGT CCGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAT
351 CAGCCTGCGG TCCGACnACA GGCCGGTTTC CTGnCGAAG CGCGGGGATT

```

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGA AAAACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCCGACC
701 GCTGTTCAA CGCCTTGGGC AGCCGCGGCT TCAGCCGCAA CGCyTGCGTC
751 GTCGTCA GTT GCGGCACGGC GGTAACGGT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCCG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGCGGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGGCGGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAATA CCGTGCGCGT
1101 GGCGGACAAC CTCGTCAATT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT...

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
1 MFSFGWVFD R PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
51 KLGGILITV RTGGKTVAVV GIGINFLPX EVENASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXXEISLR SDXRPVSXK RRDSEFLLL DGGNSRLKWA
151 WVENGTFATV GSAPYRDLSP LGAWEAKAD GNVRIVGCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTTGNAV ASGMMDAVCG SVMMMHGR LK EKTGAGK PVD VIITGGGA AK
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AEGREYEH...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311
      10      20      30      40      50      60
m311.pep MFSFGWVFD RPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGILITV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      MFSFGWAFDRPQYELGSLSPVAAALACRRALGCLGLETQIKWPNDLVVGRDKLGGILITV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTVAVVGIGINFLPXEVENAASVQSLFQTASRRGNADA AVLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTVAVVGIGINFLPKEVENAASVQSLFQTASRRGNADA AVLLLETLLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXXXXXX
g311      YAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDGRGVLHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSXKRRDSEFLLLDGGNSRLKWAVWENGTFATVGSAPYRDLSP LGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      GEISLRPDNRSVSVKRPDSEFLLLEGGNSRLKWAVWENGTFATVGSAPYRDLSP LGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIITGGGAAKVAEA					
g311	PAGKRYPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGKPVVDVIITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLNMI AEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTT
51  GCTGTGCGCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAACCGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CCGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTTGCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTTGCAA TATGCGCGGG ACGGATTTCG GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGA ACAGGAGAGG GCAAACAGAC GGTCTCAGC GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAAGCG GCGGGATTTC
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAAC GGCACGTTCC CAACCGTCGG TAGCGCGCCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCC TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 CCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCGGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGGCGCGCG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CCGTGCGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFD R PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIE TV RTGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLE TL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTV KG VDGQGVHLH LE TAEGKQTVVS GEISLRSDDR PVSVPKRDRS
201 ERFLLLD GGN SRLKWAVVEN GTFATVGSAP YRDLSPLGAE WAEKVDGNVR
251 IVGCAVCE GF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFR S RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNR H AGKRYPFPTT TGNASGMM DAVCGSVMM HGRLEKKTGA
401 GKPVDVIIT G GGAAKVAEAL PPAFLAENTV RVADNLVIH LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

```

      10      20      30      40      50      60
m311.pep  MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGIL IETV
a311      MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGIL IETV
      10      20      30      40      50      60

      70      80      90     100     110
m311.pep  RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLLXXXXXXXXX-----
a311      RTGGKTVAVVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLLETLLAELDAVLLQ
      70      80      90     100     110     120

m311.pep  -----
a311      YARDGFAPFVAEYQAANRDHGKAVLLLLRDGETVFEGTVKGV DQGQVLHLETAEGKQTVVS
      130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep  -EISLRSDXRPVSVXKRRDSE RFLLLDGGNSRLKWAWVENGTFATVGSAPYRDL SPLGAE
a311      GEISLRSDDRPVSVPKRRDSE RFLLLDGGNSRLKWAWVENGTFATVGSAPYRDL SPLGAE
      190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep  WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNH YRHPEEHGSDR
a311      WAEKVDGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNH YRHPEEHGSDR
      250     260     270     280     290

      240     250     260     270     280     290
m311.pep  WFNALGSRRFSRNACVVVSCGTAVTVDA LTTDDGHYLG GTIMPGFHLMKESLAVRTANLNR
a311      WFNALGSRRFSRNACVVVSCGTAVTVDA LTTDDGHYLG GTIMPGFHLMKESLAVRTANLNR
      300     310     320     330     340     350

      300     310     320     330     340     350
m311.pep  HAGKRYPFPTTGN AVASGMMDAVCGSVMMMHGRLKEKTGAGK PVDV IITGGGA AKVAEA
a311      HAGKRYPFPTTGN AVASGMMDAVCGSVMMMHGRLKEKTGAGK PVDV IITGGGA AKVAEA
      360     370     380     390     400     410

      360     370     380     389
m311.pep  LPPAFLAENTVRVADNLVIYGLLNMI A AEGREYEH
a311      LPPAFLAENTVRVADNLVIHGLLNLI A AEGGESEHTX
      420     430     440     450

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGCGCGA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTCAGAA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGCG GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTCA GTTCGGCTGGG CGTTTGACCG GCCGCA GTAT
451 GAGTTGGGTT CGCTGTCGCC GTTTCGCGCA CTGCGTGCC GCGCGGCTTT
501 GGGGTGTTTG GGTTCGAAA CGCAAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAACGCG TTGCCGTGGT CCGTATCGGC ATCAATTTCTG TGCTGCCCAA
651 GGAAGTGGAA AACCCGCTT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGC GGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGGTTCG CGCCATTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TGCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACTTGGA AACGGCAGaa ggCGAACAGa cggtcGtcag
951 cggcGaaaTC AGccTGCgGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggaTC GgaacgttTT tTGCTgttgg aagcggggaa cagccggctc
1051 aAGTGGgcgt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGCgCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTACG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA GCGGCATGAT
1551 GGACGCGGTT TGCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGCGCG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1 MTVLKPSHRV LAELADGLP QHVSQALAREA DMKPQQLNGF WQMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECIMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVHLHLETA GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KQWAVENGTF ATVGSAFYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHEP EHGSDRWFA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYFPFTTTGN AVASGMMDAV CGSIMMMHGR LKEKNGAGKP VDVIIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1 ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51 CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGCGCGA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTGC GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTTGACC GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGTC GGCGCGCCTT
501 GTCGCGTTTA GGTGTTGATG TGCAGATTAA GTGGCCCAAT GATTGTTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 CGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACTTGGA AACGGCAGAG GGCAACAGA CGGTGCTCAG
951 CGGCGAAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCTGTGT GCGGAGAAAT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTACG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT AGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGCG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```
1  MTLVKLSHWR VLAELADGLP QHVSQALMA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDFRPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDRWFNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPPTTTGN AVASGMMDAV CGSVMHMRGR LKEKTGAGKP VDVIIITGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*
```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
	MTLVKLSHWRVLAELADGLPQHVSQALMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR					
g311-1	MTLVKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQMPAHIRGLLRQHDGYWR					
	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVDFRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILLETVRTGGKTVAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRAGKTVAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
	QGVLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLDGGNSRLKWAVVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRVSVPKRPDSERFLLLEGGNSRLKWAVVENGTF					
	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGLAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPGLAEWAEEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL					
	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHLGGTIMPGF					
g311-1	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHLGGTIMPGF					
	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNASGMMDAVCGSVMHMRGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPPTTTGNASGMMDAVCGSVMHMRGRLEKKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

m311-1.pep VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMI AEGREYEHIX
|||||
g311-1 VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHAX
550 560 570 580 590

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

a311-1.seq

```
1 ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51 CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTTGGCGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCA GTTGGCTGGG TGTGACCG GCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA GTGGCGTGCC GCGCGCCTT
501 CTCGCGTTTG GGTGTTGAAA CGCAATCAA GTGGCCAAAC GATTGTTGCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGTCG ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GGCGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGCAGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTC TGCATTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GGCGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCTCGCGT TGCGCGGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCGCG
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCTGCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

a311-1.pep

```
1 MTVLKPSHWR VLAELADGLP QHVSQ LARMA DMKPOQLNGF WQOMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLREL GERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGEC LMFS FGWVFD RPQY
151 ELGSLSPVAA VACRRALSRL GLKTOI KWPV DLVVRGDKLG GIL IETVRTG
201 GKTVA VVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGV DG
301 QGV LHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWA VVENGTF ATVGSAPYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWL PSSAQAL GIRNHYRHPE EHGS DRWFNA LGSRRFSRNA
451 CVV VSCGTAV TVDALTDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPFPTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*
```

a311-1/m311-1 98.5% identity in 591 aa overlap

```
10 20 30 40 50 60
a311-1.pep MTVLKPSHWRVLAELADGLPQHVSQ LARMA DMKPOQLNGFWQOMPAHIRGLLRQHDGYWR
|||||
m311-1 MTVLKLSHWRVLAELADGLPQHVSQ LARMA DMKPOQLNGFWQOMPAHIRGLLRQHDGYWR
10 20 30 40 50 60

70 80 90 100 110 120
a311-1.pep LVRPLAVFDAEGLREL GERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
|||||
m311-1 LVRPLAVFDAEGLREL GERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
70 80 90 100 110 120
```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGEC	LMFSFGWV	FDRPQYELGSLSPVA	AAVACRRALSRLGL	KTQIKWPN	
m311-1	GRGRQGRKWSHRLGEC	LMFSFGWV	FDRPQYELGSLSPVA	AAVACRRALSRLGL	LDVQIKWPN	
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGIL	ETVRTGGKT	VAVVGIGIN	FVLPKEVENA	ASVQSLFQT	ASRRGNADA
m311-1	DLVVGRDKLGGIL	ETVRTGGKT	VAVVGIGIN	FVLPKEVENA	ASVQSLFQT	ASRRGNADA
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDA	VLLQYARDG	FAPFVAEYQ	AANRDHGKA	VLLLRDGET	VFEGTVKGV
m311-1	AVLLETLLVELDA	VLLQYARDG	FAPFVAEYQ	AANRDHGKA	VLLLRDGET	VFEGTVKGV
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEG	KQTVVSGE	ISLRSDDRP	SVSPKRRD	SERFLLLDG	GNSRLKWAV
m311-1	QGVHLHLETAEG	KQTVVSGE	ISLRSDDRP	SVSPKRRD	SERFLLLDG	GNSRLKWAV
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDL	SPLGAEWA	EKV DGNV	RIVGCAV	CGEFKKAQ	VQEQLARKI
m311-1	ATVGSAPYRDL	SPLGAEWA	EKADGNV	RIVGCAV	CGEFKKAQ	VQEQLARKI
a311-1.pep	430	440	450	460	470	480
	GIRNHYPHEEH	GS DRWF	NALGSR	RFSRNAC	VVSCGT	AVTVDAL
m311-1	GIRNHYPHEEH	GS DRWF	NALGSR	RFSRNAC	VVSCGT	AVTVDAL
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVR	TANLNRH	AGKRYPF	TTTTGNA	VASGMMD	AVCGSVMM
m311-1	HLMKESLAVR	TANLNRH	AGKRYPF	TTTTGNA	VASGMMD	AVCGSVMM
a311-1.pep	550	560	570	580	590	
	VDVITGGGA	AKVAEAL	PPAFLA	ENTVRV	ADNLVI	HGLLNLI
m311-1	VDVITGGGA	AKVAEAL	PPAFLA	ENTVRV	ADNLVI	YGLNMI

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTAccat cggcaTTGaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggctcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTGCGCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GCGGTGGTCA AAGCCGCGCT GGAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTTGT CGCTGGCACC GACCCCGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CGGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAGGCAGG CGTGTTGACG
1051 CTTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1  MSIQSGEILE TVKMVADRFN DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51  CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GCGCGAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTCGCCTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGTGGCGGGG
501 CGAAACCGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAATTGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTTCGGG CGATGCCGTT ATCAATGTCG GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAACCTG CTTTCAAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCCTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCGCCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCGGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAT GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CACGGTCGAG TTCGGCGGCT TGTGGGCTA
1251 CGCGCCTGTG ATGCCGCTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1  MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51  TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCXIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHGSGLAV INVGVSGPGV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTTPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGAYAPV MPVKEGSCV FVNRRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

		10	20	30	40	50	60
m312.pep	MSIQSGEILETVK	MVADQNFDVRTIT	IGIDLHDCISSD	INVLNQNIYNKI	TTVGKDLVTT		
g312	MSIQSGEILETVK	MVADRNFDVRTIT	IGIDLHDCISTD	IDVLNQNIYNKI	TTVGKDLVAT		
		10	20	30	40	50	60
		70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIV	NQRISVTPIAQIA	AATHADSYVSV	AQTLDKA	AKAIGVSFIGG	FSALV	
	:						
g312	AKHLSAKYGVPIV	NQRISVTPIAQIA	AATKADSYVSV	AQTLDKA	AKAIGVSFIGG	FSALV	
		70	80	90	100	110	120
		130	140	150	160	170	180
m312.pep	QKGMSPSDEVLIR	SIPAMKTTDIVC	SINIGSTRAGIN	MDAVKLAGETV	KRTAEITPEG		
g312	QKGMSPSDEVLIR	SVPEAMKTTDIV	CSSINIGSTRAG	INMDAVKLAGET	IKRTAEITPEG		
		130	140	150	160	170	180
		190	200	210	220	230	
m312.pep	FGCAKIVVFCNA	VEDNPF	XAGAFHGS	G--DAVINVG	SGPGVVKA	ALENSDATTL	TEVAE
g312	FGCAKIVVFCNA	VEDNPF	MAGAFHGS	GEADAVINVG	SGPGVVKA	ALENSDAVSL	TEVAE
		190	200	210	220	230	240
	240	250	260	270	280	290	
m312.pep	VVKKTAFKITR	VGELIGREASK	MNLNIPFGILD	LS--PTPPVG	DSVARILEEM	GLSVC	GTH
g312	VVKKTAFKITR	VGELIGREASK	MNLNIPFGILD	LSLAPTPAV	GDSVARILEEM	GLSVC	GTH
		250	260	270	280	290	300
		300	310	320	330	340	350
m312.pep	GTTAALALLND	AVKKGGMMAS	AVGGLSGAFI	PVSEDEGM	IXAAEAGV	LTDKLEAM	TAV
g312	GTTAALALLND	AVKKGGMMAS	AVGGLSGAFI	PVSEDEGM	IAAAEAGV	LTDKLEAM	TAV
		310	320	330	340	350	360
		360	370	380	390	400	410
m312.pep	CSVGLDMIAV	PGDTPAHTIS	GIIADEAAIG	MINSKTTAV	RIIPVTGKT	VGDTVEFG	GLLG
g312	CSVGLDMIAV	PGDTPAHTIS	GIIADEAAIG	MINSKTTAV	RIIPVTGKT	VGDSVEFG	GLLG
		370	380	390	400	410	420
		420	430	440			
m312.pep	YAPVMPVKEG	SCEVFVNR	GGRI	PAPVQSMKNX			
g312	YAPVMPAKEG	SCEVFVNR	GGRI	PAPVQSMKNX			
		430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

1	ATGAGTATCC	AATCCGGCGA	AATTTTAGAA	ACCGTCAAAA	TGGTTGCCGA
51	CCAGAATTTT	GATGTCCGCA	CCATTACCAT	CGGCATTGAT	TTGCACGACT
101	GCATCAGCAC	CGACATCGAC	GTGTTGAACC	AAAAATATTT	CAACAAAATT
151	ACCACGGTCG	GCAAAGACTT	GGTGCGCGCA	GCAAAATATC	TGTCTGCCAA
201	ATACGCGCTG	CCGATTGTGA	ATCAGCGCAT	TTCTGTCAAG	CCGATTGCCC
251	AAATCGCGGC	GGCCACCCAT	GCTGATTCTT	ACGTCAGCGT	GGCGCAAAC

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301 TTGGATAAGG CTGCCAAAGC CATCGGCGTG TCTTTTATTG GCGGCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTCGCCTTC TGACGAGGTG TTAATCCGTT
401 CCATTCCCGA AGCGATGAAG ACTACTGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGTA CGCGCGCCGG TATCAATATG GACGCGGTCA GACTGGCGGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACTAGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTATGGCG
601 GGCGCGTTTC ACGGCTCAGG CGAAGCGGAT GCTGTGATTA ATGTCGCGCT
651 ATCCGGCCCG GGTGTCGTAA AAGCCGCGTT GGAAAATTTCG GATGCAACGA
701 CATTGACCGA AGTTGCCGAA GTTGTGAAGA AAACCGCCTT CAAAATTACC
751 CGCGTGGGCG AACTCATCGG CCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTTGGTATT CTCGACTTGT CGCTGGCACC GACCCCTGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGTT TGAGCGTCTG CGGTACGCAC
901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCGAGCGCGG TTGGCGGTTT GAGTGGCGCG TTTATCCCGG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAAGCAGG CGTGCTGACG
1051 TTGGATAAAC TCGAAGCGAT GACCGCCGTT TGTTCCGGTCG GCTTGGATAT
1101 GATTGCCGTT CCCGGCGACA CACCCGCGCA CACCATTTC GGCATCATTG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC TGCCGTGCGC
1201 ATTATTCCGG TAACCGGTAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 CCTGTTGGGC TACGCGCTG TAATGCCGGT AAAAGAAGGC TCATGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCC CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1306; ORF 312.a>:

```

a312.pep
  1 MSIQSGEILE TVKMOVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
 51 TTVGKDLVAT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQ
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP VVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCPTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTGV DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

m312/a312 96.7% identity in 451 aa overlap

```

          10      20      30      40      50      60
m312.pep  MSIQSGEILETVKMOVADQNF DVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       MSIQSGEILETVKMOVADQNF DVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT
          10      20      30      40      50      60

          70      80      90     100     110     120
m312.pep  AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAKAIGVSFIGGFSALV
          70      80      90     100     110     120

          130     140     150     160     170     180
m312.pep  QKGMSPSDEVLIRSIPEAMKTTDIVCXNIGSTRAGINMDAVKLAGETVKRTAEITPEG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       QKGMSPSDEVLIRSIPEAMKTTDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITLEG
          130     140     150     160     170     180

          190     200     210     220     230
m312.pep  FGCAKIVVFCNAVEDNPFMAGAFHGS--DAVINVGVS GP VVKAALENS DATTLTEVAE
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS GP VVKAALENS DATTLTEVAE
          190     200     210     220     230     240

          240     250     260     270     280     290
m312.pep  VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCPTH
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a312       VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCPTH

```

720

	250	260	270	280	290	300
m312.pep	300	310	320	330	340	350
	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
m312.pep	360	370	380	390	400	410
	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc cgcgcaccta cggatcgggc aatcccggcg cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 cgcgcaaaag tttggttgcc gttttgcttg cagcgctgct tcaagaaccg
151 ctcggtttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taagggcggc aaaggcgtgg
251 caacggcatt gggcgtgctt ctggcactct ctcccgcaac tgccttggtc
301 tgcgcgttga tttggcttgt gatggcattc ggcttcaaag tatcctccct
351 tgccgcgctg gtcgccacaa ccgccgcccc ccttgccgca ctgtttttaa
401 tgccgcatac ttcttggtt ttcgcaaccc tcgcaatcgc catattgggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYGS G NPGATNVLR S GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPFVFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNI LN LIKGESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTGTCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGCTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCGCAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTC GGCTTCAAGG TGTCTCCCTT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTGCGCCGA TCCTTCTTTA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYGS G NPGATNVLR S GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPFVFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVS WV WATVAIALLV
151 LFRHKSNI VK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313 .pep	MDDPRTYSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
g313	MDDPRTYSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313 .pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313 .pep	TATIAAPVAASFFMPHVS VWVATVAIALLVLFHRKSNIVKLLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

1	ATGGACGACC	CGCGCACCTA	CGGATCGGGC	AATCCGGGGG	CAACCAATGT
51	TTTACGCAGC	GGCAAAAAAA	AGGCGGCCGC	GCTGACGCTC	TTGGGCGATG
101	CCGCCAAAGG	TTTGGTTGCC	GTTTGTGCTG	CACGCGTGCT	TCAAGAACCG
151	CTCGGTTTAT	CCGACAGCGC	AATCGCGGCC	GTGCGACTCG	CCGCGCTGGT
201	CGGGCATATG	TGGCCGGTGT	TTTTCCGGATT	TAAAGGCGGC	AAAGGCGTGG
251	CAACGGCATT	GGGCGTGCTT	CTGGCACTCT	CTCCACAAC	TGCCTTGCTC
301	TGCGCGTTGA	TTTGGCTTGT	GATGGCATTG	GGCTTCAAGG	TGTCTCCCT
351	TGCCGCATTA	ACCGCCACAA	TCGCCGCCCC	CCTTGCCGCA	CTGTTTTTTA
401	TGCCGCATAC	TTCTTGATT	TTCCGAACCC	TCGCAATCGC	CATATTGGTG
451	TTGCTCCGCC	ATAAGAGCAA	CATCCTCAAC	CTGATTAAAG	GCAAAGAAAG
501	CAAAATCGGC	GAAAAACGCT	GA		

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

1	MDDPRTYSGS	NPGATNVLRS	GKKKAAALT	LGDAAKGLVA	VLLARVLQEP
51	LGGLSDSAIAA	VALAALVGHM	WPVFFGFKG	KGVATALGV	LALSPTTALV
101	CALIWLVMF	GFKVSSLAAL	TATIAAPLAA	LFFMPHTSWI	FATLAIAILV
151	LLRHKSNILN	LIKGESKIG	EKR*		

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
a313	MDDPRTYSGNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPTTALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVS VWVATVAIALLVLFHRKSNIVKLLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgattgtggt
 51  cacgctgctt gtagtcagtg tcggtctggt gattgaagtt gtgcccttgg
101  cctttaccaa ggcggcaaca cagccggcgc cgggcgtgaa gccttacaa
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcgttacg
251  gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
301  gggtccaaac gtaccggtcc tgatttgga cgtgtgggcg gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcatcc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551  agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEK IGVLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMFAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAA
151  GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTG GTCCGTTCCG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTGCGGGA GAGTCGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEK IGVLIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMFAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401
      10      20      30      40      50      60
m401.pep  MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||
g401      MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||
      10      20      30      40      50      60
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
```


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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
g401      HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1   ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGGGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTG GTCCGTTCCG TCGGGAAACC GAGCGTTACG
251 GTCATTACTC TGTGCGCGGA GAGTCGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTG CCGTGCTTGG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1   MKLQQLAEK IGVLVFTLL VSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401.pep  MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
a401      MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
          70      80      90      100     110     120

          130     140     150     160     170     180
m401.pep  HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          |||||
a401      HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIAKAPEALA
          130     140     150     160     170     180

          190     200
m401.pep  NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaataact agtgtgatta atatgctttc
51  tttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTTTC atttattcctt
151 gcctGtttttc tgACCGgtat cgcgcgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATTT TCCCACTTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTATCGGC TTTGTGATAC TTGATTtgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTCT GCTGctgtcc
551 cTTTGTTTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTAC TGCCGGATTc
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCAACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGCT
901 GCCATCCCG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgetTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCctt AATAAAGAAC
1301 TGCTCaagca aCGCCTTTcc cgGTTGATTT GGCCGAAAG CGGCAGgcac
1351 gtATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAGG TTgtctctCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPOAFSFL
51  ACFLTGIAGV AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS
301 AIPQMISMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDA AOKVVSRLMI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGCnTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACCCCTT
151 GCTGTTTTTC TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTG
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsA sGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTTTCG CAmCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTATCGGC TTTGTGATAC TTGATTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TwTGATTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTT CAAAAAAGTC TCCGACTGAA TGCAGTGTcG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTyTAC TGCCGGATTc

```

```

651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TagGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTATTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAATATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGTAT AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCAGG ATTTTAAAA CAGGTGCAAA
1151 GCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCGTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
51 ACFLTGI AVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLMI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPAQAFSFTLACFLTGI AVG					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPAQAFSFI LACFLTGI AVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQIYLLICXIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					

726

```

g402      |||||:|||||
          250      260      270      280      290      300
          |||||
          310      320      330      340      350      360
m402.pep  AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          |||||
g402      AIPQMISMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
          310      320      330      340      350      360
          |||||
          370      380      390      400      410      420
m402.pep  NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          |||||
g402      NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
          370      380      390      400      410      420
          |||||
          430      440      450      460      470      480
m402.pep  VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTDAAAQKVVSRLMIQMTPEPSAGAE
          |||||
g402      VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTDAAAQKVVSRLMIRMTEPSAGAE
          430      440      450      460      470      480
          |||||
          490
m402.pep  VITDDNMIVEYKYGRGIX
          |||||
g402      VITDDNMIVEYKYGRGI
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGCTTTT
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTCCTGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGACAG CGCTTTGTTG ATATTCCTCT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGAGTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTCCTCCG GCTTCGTTCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTCCAATG TTTATTCGCG CAACGTTGCC
451 GGCAGTGCA TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTCTCT
501 GTCCACCAA CAGATTTACC TGCTCATCTG TTTGATTCTT GCTGCTGTCC
551 CTTTGTTCG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTCTCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTCTAC TGCCGGATTG
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTATATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTG GGCCGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCCT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTPKNT SLIYMLSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL

```

51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDLRI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFVVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLMI QMTEPSAGAE VITDDNMIVE YKYGRGI*

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPPQAFSFTLACFLTGIAVG					
a402	MDIVNTKPNTSLIYMLSFLSGLLSLGIEVLWVRMFSFAAQSVPPQAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDLRIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDLRIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFVVGLSTGSWARVLS					
a402	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFVVGLSTGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHDPDEKFDLILM					
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHDPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLMIQMTEPSAGAE					
a402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVVSRLMIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGTTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAT
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSAGGLTG LTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIQPYGNHTG NSAPSV EADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAT
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCGAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK

```

```

51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSV	FILSACGTLTG	IPSHGGGKRFA	VEQELVAASARA	AVKMDLQALHGR	
	:	:	:	:	:	:
m406	MQARLLIPILFSV	FILSACGTLTG	IPSHGGGKRFA	VEQELVAASARA	AVKMDLQALHGR	
	:	:	:	:	:	:
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQ	SGSLTGGRY	SIDALIRGEY	INSPAVRTDY	TYPREYETTA	ETTSGLTG
	:	:	:	:	:	:
m406	KVALYIATMGDQ	SGSLTGGRY	SIDALIRGEY	INSPAVRTDY	TYPREYETTA	ETTSGLTG
	:	:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTSLSTLNAPAL	SRTQSDGSG	SRSSLGLN	IGMGDYRNET	LTNPRDTAFL	SHLVQTVF
	:	:	:	:	:	:
m406	LTSLSTLNAPAL	SRTQSDGSG	SKSSLGLN	IGMGDYRNET	LTNPRDTAFL	SHLVQTVF
	:	:	:	:	:	:
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVS	PANADTDV	FINIDVFGT	IRNRTEMH	LYNAETLKA	QTKLEYFAV
	:	:	:	:	:	:
m406	FLRGIDVVS	PANADTDV	FINIDVFGT	IRNRTEMH	LYNAETLKA	QTKLEYFAV
	:	:	:	:	:	:
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEA	AYKENYAL	WMPYKVS	IGIKPTEGL	MVDFS	SDIQPYGNHT
	:	:	:	:	:	:
m406	IKPKTNAFEA	AYKENYAL	WMPYKVS	IGIKPTEGL	MVDFS	DIRPYGNHT
	:	:	:	:	:	:
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDE	AVRQHRQGPX				
	:	:				
m406	SHEGYGYSDE	VVRQHRQGPX				
	:	:				
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACCTC
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAACCT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCTC GATATCCAAC
851 CATACGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 ACTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
  1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
  51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
 101  DYTYPYRSETT AETTSGLTGLT LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
 151  IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
 201  IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
 251  AYKENYALWM GPYKVSCKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301  SHEGYGYSDE AVRRHRQGQP *

m406/a406  98.8% identity in 320 aa overlap

      10      20      30      40      50      60
m406.pep  MQARLLIPILFSVFILSACGLTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR
          |||
a406      MQARLLIPILFSVFILSACGLTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR
      10      20      30      40      50      60

      70      80      90     100     110     120
m406.pep  KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPYRSETTAETTSGLTGLT
          |||
a406      KVALYIATMGDQSGSGLTGGRYSIDALIRGEYINSPAVRTDYTYPYRSETTAETTSGLTGLT
      70      80      90     100     110     120

      130     140     150     160     170     180
m406.pep  LTTSLSTLNPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF
          |||
a406      LTTSLSTLNPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF
      130     140     150     160     170     180

      190     200     210     220     230     240
m406.pep  FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
          |||
a406      FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
      190     200     210     220     230     240

      250     260     270     280     290     300
m406.pep  IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTGLMVDFS DIRPYGNHTGNSAPSVEADN
          |||
a406      IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTGLMVDFS DIQPYGNHMGNSAPSVEADN
      250     260     270     280     290     300

      310     320
m406.pep  SHEGYGYSDEVVRQHRQGQFX
          |||
a406      SHEGYGYSDEAVRRHRQGQFX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
  1  atggctcgac ggacctgac cgcagatacc gacatatttg ttctgcttgc,
 51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```



```

101 tcgtcaaacg attcggacac caagccgctg tctcggtcga ggccgaggggt
151 cagctgggtc atgtcgttcg agccgatgga gaagccgctg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301 aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 cgacgttggt cagaccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgctgccgc
501 cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601 tttatcgacg tagaagtcga caggggatgc gtaaccggcg atcgccgga
651 taatttcgcg tttcagttcg tcgtcttgtt tgtcaaattc caacaaggct
701 ttcgggtgga tgcgatttg gcggttgatg ataaattcca tacgcgcaa
751 gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851 gcgacatcgg taatttgtag gtccagcagg ccggcataga taaagccggt
901 atcgccctcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951 cggtcgcatt gccgcagccg acgacggcag gaatacccg ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgccg cggttggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccattc cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgcacaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttggga tttgacgggt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 accatggtc ttgcgcagga tggcggttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 ccagaccgt aagaggaggt aacaaagacg acttggttgt agccgattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTDAT DIFVLLAAGG DGKMQHHFDG RVAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFFGAQSA DERNHDFDVG QTHFVTNAFO GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAAADQV GVFGVFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAGQIGE AECEFGIADV HHDGDFGCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHGDDG
351 STFHHGFPIR IGHVGNQYVA GFDGIHLGSI FNQAHLLALTD FLTDGTTFAQ
401 DGFFAVDVA AQVAAAFFLG FDGFGAGLQD VEFVAVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVGNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGGF ACFERGF EHI KFRVRDRALY DVFAQTVRGG NKDDLTVVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaaggcga gatggcaagg tgcagcatca ctttgacggc aggggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggtcga gaccgaggggt
151 cagttgggtc atgtcgttcg agccgatgga gaagccgctg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggg caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acggtgccgc
501 cgaccaggtt ggcgtattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601 tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttcgcg ttttaattcg tcgtcttgtt tgtcaaattc caacaargct

```

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact tttacaggtg ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgccctcg gcacaggata cggttaactt ttgaccgttt ttcagcaatt
951 cgggttgcat gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgcgg cggttggtta cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgcggttga tggcgaagcg gcgcagggtg cggttgacct
1251 cttcttgagg ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctacagtaatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatggtt ttacgcagga tggcgggctt gccgytttg agcgtgggtt
1551 tgaacacatr aaattcgtcc ggggtgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1   MVGXALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF ROYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNNG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFVGVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QQXFGVDTDL AVDDKFHTRO
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351 STFHHGFPIR IGHVGNEYVA GFDGIHLGSI FNQAHALTD FLTDAFAFAX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVGNGE AVAVFLGDID VGYGFTGFCE VGKNHFDVFX
501 THGFTQDGLL ARFERGFEHX KFVRVDRPLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

```

m501/g501
      10      20      30      40      50      60
m501.pep  MVGXALTADADI FVLLAAGGDGKVQHFFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG
          ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      MVGRTLTAADTDIFVLLAAGGDGKMQHFFDGRFAFVKRFGHQAAVSVEAEGQLGHVVRADG
          10      20      30      40      50      60

      70      80      90     100     110     120
m501.pep  EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGF DNGFGFAQSADERNHDFNNG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG
          70      80      90     100     110     120

      130     140     150     160     170     180
m501.pep  QPHFIADAFQGF AFAFQGETVFEVVDITRRTTEAQHRVFFMR FVYVAADQVGVFGFVGVGH
          | |||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      QTHFVTNAFQGF AFAFQGETVFEALGNITRRTTEAQHRVFFMR FVYVAADQVGVFGFVGVGH
          130     140     150     160     170     180

      190     200     210     220     230     240
m501.pep  TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

733

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLFVKFQQGFVRVDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDIFYRCFRHIVXGDIIGNLYVQQTGIDKAG
g501	AVDDKFHTRQADAFAGQIGAECEFGIADVHHDIFYRCFRHIVXGDIIGNLYVQQTGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTVFQQFGCIAAADNGRNASQFTRDDGGVAGTAAAVGNDGRSTFHHGFPIR
g501	IAFGTGYGNFLTVFQEFGRIAAADNGRNTQFARDDGGVAGASAAVGHGDSSTFHHGFPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGAAFA XYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQAH LALTD FLTDGTTFAQDGF FAVDGVAAQVA AAF FLG
	370 380 390 400 410 420
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVMRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQVVCQLGDF FVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGGGLARFERGFEXXKFVRVDRTLVDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXIKFVRVDRALVDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVGEHEHT
g501	NKDDLIVVAGFGVGEHEHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq (partial)

1	ATGGT	TCGGAC	GGGCCT	TGAC	CGCAGAT	GCC	GACATATTTG	TTCTGCTTGC
51	GGCAGG	CGGA	GATGGCA	AAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT	
101	TCGTCAA	ACG	ATTCGG	AATAC	CAAGCCGCTG	TCGCGGTCGA	GACCGAGGGT	
151	CAGTTGGG	TTC	ATGTCG	TTCG	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA	
201	GGAATTG	TTC	CGCCAAT	ATACC	CGGTTGCTCG	GCAGCTCGCA	CATCATAATC	
251	AGGCGC	AGGC	CGTTTT	TGCC	CGGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT	
301	GACAAC	GGCT	TCGGCT	TTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT	
351	CAACGT	TGGT	CAACCC	CATT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT	
401	TCCAAG	GCGA	AACAGT	CTTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC	
451	ACGGA	AAGCCC	AACATC	GGGT	TTTCTTCATG	CGGTTTCGTAT	ACGTTGCCGC	
501	CGACC	AGGTT	GGCGT	ATTCG	TTGGATTTGA	AGTCGGACAT	ACGGACGATG	
551	GTTTT	TACGCG	GATAA	ACCGA	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT	
601	TTTAT	CGACG	TAGAAG	TCGA	CAGGGGACGC	GTAACCGGCG	ATACGGCGGG	
651	TAATTT	CCGC	TTTAA	TTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT	
701	TTGGGG	TGGA	TACCG	ATTG	CGGTTGATG	ATAAATTCCA	TACGCGCCAA	
751	GCCGAT	GCCT	TCGCT	TGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCGGAT	
801	TGCCG	ACGTT	CATCAT	GACT	TTTACAGGTG	CTTTAGGCAT	GTTGTCCAAA	
851	GCAAC	ATCGG	TAATTT	GTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT	
901	ATCGC	CTTCG	GCACAG	GATA	CGGTAAC TTC	TTGACCGTTT	TTCAGCAATT	
951	CGGTT	TGCATT	GCCGC	CAGCCG	ACAACGGCAG	GAATACCCAG	TTGCGCGCGC	

```

1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTGCGACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGCTGCCTT
1251 CTTCTTGGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGTTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGATC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGGTCGT AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1  MVGRALTADA DIFVLLAAGG DGKVQHHFDG RVAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH VVQSNIGNLY VQQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFFAVDRKA AQVAAFFFLG FDGFGTGLQD VEFVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVGNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTGTG
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFEVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGFEVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQGFGVDTDL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVXGDNIGNLYVQQTGIDKAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTVFQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFP					
a501	IAFGTGYGNFLTVFQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFP					
	310	320	330	340	350	360

	370	380	390	400	410	420
m501.pep	IGHVGNEXYVAGFDGIHLGSI FNQAH LALTDFLT DGA AFAXYGFVAVDGEAAQVAVALFLG					
	: : : : : : : : : :					
a501	VGHVGNQYVAGFDGIHLGSI FNQAY LALTDFLT DGA AFAQDGGFFAVDRKAAQVAAAFLLG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGCQVMRQLSNFFVGNGEAVAVFLGDIID					
	: : : : : : :					
a501	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGCQVMRQLGDFVFNGEAVAVFFGDIID					
	430	440	450	460	470	480
	490	500	510	520	530	540
m501.pep	VGYGFTGFCFVGKNHFDVFXTHGFTQDGG LARFERGF EHXKFVRVDRTLYDVFAQTVRGG					
	: : : : : : : : : : : : : :					
a501	VGYRFAFGFCFVGKNHFDVFXAHGFAQDGRFACFQRGF EHFVGDICALYDVFAQTVGXS					
	490	500	510	520	530	540
	550	559				
m501.pep	NKDDLIVXGFGVEGEHHTX					
	: : : : :					
a501	DKDDLVTGFGFIEGHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 1337>:

g502.seq	1	atgatgaaac	cgcacaacct	gttccaattc	ctcgcggttt	gtcccttgac
51	cgtcgccgtc	gcttcgcgac	aggcggggcg	ggtggacgcg	ctcaagcaat	
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	aaccgtocaa	
151	agcaaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tcctgcgccc	
201	gggcctcttc	aaattgggaat	acagcttgcc	ctacagacag	actattgtcg	
251	gcgacggtca	aaccgttttg	ctctacgatg	ttgatttggc	acaagtgacc	
301	aagtcgtccc	aagaccaggc	catcggcggc	agccccgccg	ccatcctgtc	
351	gaacaaaacc	gccctcgaaa	gcagttacac	gctgaaagag	gacggttcgt	
401	ccaacggcat	cgattatgtg	cggggcaacg	cccaaacgca	acaacgccgg	
451	ctaccaatac	atccgcacgc	gcttcaaagg	cggcaacctc	gccgccatgc	
501	aqcttaa					

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

g502.pep

1	<u>MMKPHNLQFQ</u>	<u>LAVCSLTVAV</u>	<u>ASAQAGAVDA</u>	LKQFNNDADG	ISGSFTQTQVQ
51	SKKKQTQAHG	TFKILRPLGF	KWEYTLPYRQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNTK	ALESSYTLKE	DGSSNGIDYV	RGNAQTQORR
151	LPIHPHRLOR	ROPRRHAA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

```
m502.seq
1  atgatgaaac cgcacaacct gttccaattc ctgcgcgttt gtcctctgac
51  cgtcgccgtc gcttcgcgac agggcgggcg ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggg atcagcggga gcttcaccca amccgtocaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tcctgcgacc
201 gggccttttc aaatgggaat acaccaaat t.agaggcaa accatcgctc
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcgc ccatcctgtc
351 gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgccggcta
451 ccaatacatc cgcacggtc tcaaaggcgg caacctcgcc gccatgcage
501 tyaa
```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

m502.pep

1	<u>MMKPHNLFQF</u>	<u>LAVCSLTVAV</u>	<u>ASAQAGAVDA</u>	LKQFNNDADG	ISGSFTQXVQ
51	XKKKTQTAHG	TFKILRPGLF	KWEYTKLYRQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGX	SPAAILSNKX	ALESSYTLKE	DGSSNGIDYV	GNAQTQORRL
151	PIHPHRLQRR	QPRRHAAX			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPRQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502 . seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGTCG	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCGC	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502 . pep

1	MMKPHNLFQF	LAVCSLTVS	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKKTQTAHG	TFKILRPGLF	KWEYTSFYKQ	TIVGDGQTVW	LYDVLDAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVAASQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSFYKQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAAX					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```
1 ATGatGAAAc cgcaCaacct gttccaaTtc CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTGG CTCTACGATG TTGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCAAA
601 GCGTGGACG TGTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```
1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTLPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```
1 ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGCGGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCAAA
601 GCGTGGACG TGTGAGCAA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```
1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*
```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG					
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF					
	130	140	150	160	170	180

```

                190      200
m502-1.pep    GGLNTPQLSRGAFKFTPPKGV DVL SNX
                |||
g502-1        GGLNTPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGCGGCG AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GGCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCGCCCCAAA
601 GCGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTSYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNTK ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTISIF GGLNTPQLS  RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep    MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                |||
m502-1        MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep    TFKILRPGLFKWEYTSYKQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNTK
                |||
m502-1        TFKILRPGLFKWEYTKPYRQTIIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNTK
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep    ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                |||
m502-1        ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                130     140     150     160     170     180

                190     200
a502-1.pep    GGLNTPQLSRGAFKFTPPKGV DVL SNX
                |||
m502-1        GGLNTPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcgaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

1	atgtcgcgac	cgccgggcac	ggcaaccatt	ttgttccatg	ccgcttcgat
51	ttcgggcacg	agctgttcgg	ggaaaggcgt	atccaaaatc	cattggcgga
101	tttctttgcc	gacgcgtgcc	agttcggcaa	cgtcttcgac	atccaatatt
151	gccagtcgcg	cggaaatgcg	ttcgcctcaga	ccgttgtgtg	cgaggaatgc
201	gcagtaag				

m503.pep

1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTS NF
51 ASAAEMRSLR PLCARNAR*

Homology with a predicted ORF from *N. gonorrhoeae*

m503/g503

```

              10      20      30      40      50      60
m503.pep    MSAPPASATILFHAASISASSCSGKGVSKIHWRLSLPTRASSATSSTSNFASAAEMRSLR
            ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|
g503        MSAPSASVIILFHAASISASSCSGKGVSKIHWRLSLPTRASSETSTSNFARAAEMRSFR
              10      20      30      40      50      60

              69
m503.pep    PLCARNAR
            |||||
g503        PLCARNAR

```

a503.seq

1	ATGTCCGCGC	CGCCGGCATC	GGCAACCATT	TTGTTCCATG	CCGCTTCGAT
51	TTCGGCATCG	AGCTGTTCTG	GGAAGGGCGT	GTCCAAAATC	CATTGGCGGA
101	TTTCTTTGCC	GACGCGTGCC	AGTTCGCGAA	CGTCTTCGAC	ATCTAATTTT
151	GCCAGTGC	CGGAAATGCG	TTCGCTCAGA	CCGTGTGTG	CGAGGAATGC
201	GCGGTAG				

a503.pep

```

1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
51 ASAAEMRSLR PLCARNAR*

```

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRLSLPTRASSATSSSTSNFASAAEMRSLR
          |||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRLSLPTRASSATSSSTSNFASAAEMRSLR
          10      20      30      40      50      60

```

	69
m503.pep	PLCARNARX
a503	PLCARNARX

g503-1.seq

1	ATGGCGCGG	CGTTGTACAG	GGAGGCGAAA	ACGTGGCGCA	TCGCTTTTTT
51	AACGCTATCC	AAGCCATTGA	TATTCAGGAA	GGTTTCTCTG	TGCCCGGGCAA
101	ATGATCGCTC	CGGCAAGTCT	TCGGCGGTTG	CGGAAGAGCG	TACGGCAACG
151	GAAATGCTCC	CGCCGTCGGC	ATCGGTAATC	ATTTTGTTC	ATGCCGCTTC
201	GATTTCCGCA	TCGAGCTGTT	CGGCGAAGGG	CGTGTCCAAA	ATCCATTGGC
251	GGATTTCCTT	CCGCAAGCGT	CGCAGTTCGG	AAACGCTCTC	GACATCCAAT
301	TTTGCCAGAG	CGGCGGAAAT	GCGTTCGTTG	AGACCGTTGT	GTGCGAGAAA
351	TGCGCGGTAG				

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep

```

1  MARSLYREAK TWRI AFLTSL KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSETSSTSN
101 FARAAEMRSF RPLCARNAR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51 AACGTTATCC AAGCCGTTGA TGTTCAAGAA GGTTCCTGT TGTCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTTCGGC TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGCGCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep

```

1  MARSLYREAN TWCIALTSL KPLMFKKVSC CPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*
```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRI AFLTSLKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI					
	:					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60

	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWIRISLPTRASSETSSTSNFARAAEMRSFRPLCARNARX					
	:					
m503-1	ILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51 AACGTTTTC AAGCCGTTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTTCGGC TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGCGCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*
```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
	:					
m503-1	MARSLYREANTWCIALTSLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60

	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	:					
m503-1	ILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```
g504.seq
1  atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgccacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgtgta ccgcattccg gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctgggtgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggtatg aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgccgggtgc gcttttggtc tatctcggct cggatttggt
1101 ggttttgggt acagtattta tgttttatgt gcccaaaaaa cgggcgtggg
1151 tattgttttc aaacdgcata atccgttttg ctatgtcttc ggccgcagc
1201 gaacgggatt tgcagaagga atttcaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga
```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```
g504.pep
1  MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLLS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPPK RAWVLFSENKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```
m504.seq..
1  atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgatttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgcaccat ccgcgtgaac
151 catcctttga ccttgccacgg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccg gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggaaacg gattattttt
551 ggattaccgg cacgcgcagc ggcttgacgc agcaataacc ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctgggtgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttggtatg aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgtc gggtttgag
```

```

1051 atgacccggt ccccggtg gcttttggc tatctcggc cggtgctgtt
1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgacgc
1201 gaacgggatt tgcagaagga atttcaaaa cacgtcgaga gtctgcaacg
1251 gctcggcaag gacttgaatc atga

```

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

```

1 ILVQDLPEFEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLQLDGF SEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

m504.pep	10	20	30	40	50	60
	ILVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
g504	MLVQDLPEFEVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
m504.pep	70	80	90	100	110	120
	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
g504	YQASFADGGSDLTFKAWNLRDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	130	140	150	160	170	180
	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
g504	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPILQDK					
	130	140	150	160	170	180
m504.pep	190	200	210	220	230	240
	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI					
g504	DYFWLTGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
m504.pep	250	260	270	280	290	300
	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR					
g504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKGQQDKMQGYFYEMLYGVMNAALDETIR					
	250	260	270	280	290	300
m504.pep	310	320	330	340	350	360
	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTSPGALLV					
g504	RYGLPEWQQDEARNRFLHLSMDAYTGLTEYPAPMLQLDGFSEVRSSGLQMTSPGALLV					
	310	320	330	340	350	360
m504.pep	370	380	390	400	410	420
	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK					

743

g504 YLGSVLLVLGTVFMFYVPPKKRAWVLFNSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
 370 380 390 400 410

m504.pep DLNHD
 |||||
 g504 DLNHD
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504.seq
 1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAA AATTCCATAT
 51 CGATTTTAC AATACGGGTG TGCCGCGCGA TTTTGCCAGT GATATTGAAG
 101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
 151 CATCCTTTGA CCTTGACGCG CATCACGATT TATCAGGCGA GTTTTGCCGA
 201 CGGCGGTTCG GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
 251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
 301 ATTGGCAAAC ACAATATATC TCTTGAGTTC GATCAGTTTA CTTCTATGAA
 351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAAGC CTGAAATCCA
 401 CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
 451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
 501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
 551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT
 601 ATCCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
 651 GTTTTTGAAA GATGGGGAAG GGCGCAAACG TCTGGTTGCC GACGCAACCA
 701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCGGAAAAAC
 751 ACGCTGAACA TCTTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
 801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
 851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGATGA AACCATACGC
 901 CCGTACGGCT TGCCCCAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
 951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
 1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGCAG
 1051 ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CCGTGCTGTT
 1101 GGTATTGGGT ACGGTATTGA TGTTTTATGT GCGCGAAAAA CGGGCGTGGG
 1151 TATTGTTTTC AGACGGCAAA ATCCGTTTTG CCATGTCTTC GGCCCGCAGC
 1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
 1251 GCTCGGCAAG GACTTGAATC ATGACTGA

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504.pep
 1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTL
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQOD EARNRFLLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

m504/a504 99.8% identity in 425 aa overlap

	10	20	30	40	50	60
m504.pep	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRNVHPLTLHGITI					
a504	ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLETRIRNVHPLTLHGITI					
	10	20	30	40	50	60
m504.pep	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
a504	YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED					
	70	80	90	100	110	120
m504.pep	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
a504	MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ					
	130	140	150	160	170	180
m504.pep						

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```

a504      |||||
MSEGAEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
          130      140      150      160      170      180

          190      200      210      220      230      240
m504.pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          |||||
a504      DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          190      200      210      220      230      240

          250      260      270      280      290      300
m504.pep  REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          |||||
a504      REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          250      260      270      280      290      300

          310      320      330      340      350      360
m504.pep  RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          |||||
a504      RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          310      320      330      340      350      360

          370      380      390      400      410      420
m504.pep  YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
          |||||
a504      YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK
          370      380      390      400      410      420

m504.pep  DLNHDX
          |||||
a504      DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1  atgtttcggt tacaattcag gctgtttccc cctttgcgaa cgcgatgca
51  catcctgttg accgccctgc tcaaatgcct ctccctgtcg tcgctttcct
101 gtcgtcacac gctgggaaac cggctcggac atctggcggt ttacctttta
151 aaggaagacc gcgcgcgcac cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacgggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttggaact tgcccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cggtagacac ctgggaacac gtgcagcagg ctttggaaca
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagg tacgatttgg
401 gcggacgcta catcagccag cagcttcctg tccacctgac cgccatgtac
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cggccaccgg catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccaccac
601 gtcccttctc cgcaggaagg cggcggcggt tggcgaggatt ttttcggcaa
651 acctgcatac accatgacac tggcggaaca attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccagcgg acaaaggcttc
751 gtgttgacac tccgccccgt ccaaggggaa ttgaacggca acaaagccca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1  MFRLOFRLFP PLRTAMHILL TALLKCLSLI SLSCSLHTLGN RLGHIAFYLL
51  KEDRARIVAN MRQAGLNPDV QTVKAVFAET AKCGLELAPA FFKKPEDIET
101 MFKAHVHWEH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHILTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTGIQG VKQIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDGQGF
251 VLHIRPVQGE LNGNKAHDA VFNRNTEYWI RRFPTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

m505.seq (partial)

```

1  GGCATGTTTC  GTTTACAATT  CAGGCTGTTT  CCCCCTTTGC  GAACCGCCAT
51  GCACATCCTG  TTGACCGCCC  TGCTCAAATG  CCTCTCCCTG  CTGCCGCTTT
101 CCTGTCTGCA  CACGCTGGGA  AACCGGCTCG  GACATCTGGC  GTTTTACCTT
151 TTAAAGGAAG  ACCGCGCGCG  CATCGTCGCC  AATATGCGGC  AGGCGGGTTT
201 GAACCCCGAC  CCCAAAACGG  TCAAAGCCGT  TTTTGCGGAA  ACGGCAAAAG
251 GCGGTTTGGA  ACTTGCCCCC  GCGTTTTTCA  GAAAACCGGA  AGACATAGAA
301 ACAATGTTCA  AAGCGGTACA  CGGCTGGGAA  CATGTGCAGC  AGGCTTTGGA
351 CAAACACGAA  GGGCTGCTAT  TCATCACGCC  GCACATCGGC  AGCTACGATT
401 TGGGCGGACG  CTACATCAGC  CAGCAGCTTC  CGTTCCCGCT  GACCGCCATG
451 TACAAACCGC  CGAAAATCAA  AGCGATAGAC  AAAATCATGC  AGGCGGGCAG
501 GGTTCGCGGC  AAAGGAAAAA  CCGCGCCTAC  CAGCATACAA  GGGGTCAAAC
551 AAATCATCAA  AGCCCTGCGT  TCGGGCGAGC  AACCATCGTC  CTGCCCGACC
601 ACGTCCCCTC  CCCTCAAGAA  GCGGGGGAAG  GCGTATGGGT  GGATTTCTTC
651 GGCAAACCTG  CCTATACCAT  GACGCTGGCG  GCAAATTGTT  CACACGTCAA
701 AGGCGTGAAG  ACCCTGTTTT  TCTGCTGCGA  ACGCCTGCCT  GGCGGACAAG
751 GTTTCGATTT  GCACATCCGC  CCCGTCCAAG  GGAATTGAA  CGGCGACAAA
801 GCCCATGATG  CCGCCGTGTT  CAACCGCAAT  GCCGAATATT  GGATACGCCG
851 TTTTCCGACG  CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

m505.pep (partial)

```

1  MFRLQFRLFP  PLRTAMHILL  TALLKCLSL  LPLSCLHTL  GNRLGHLAF  YLLKEDRAR  IVAN
51  KEDRARIVAN  MRQAGLNPD  PKTAVKAVF  AETAKGGL  ELAPAFFRK  PEDTETMF  KAVHGW
101 MFKAVHGW  EHVQQALDK  HEGLLFIT  PHIGSYDL  GGRYISQ  LPPFLTA  MYKPPK
151 KPPKIKAI  DKIMQAGR  VVRGKGK  TAPTSTI  QGKQIMQ  AGRVVRG  KGKTA
201 VPSPOEG  GEGVWVD  FFGKPA  YTMTLA  AXLAHV  KGVKTL  FFCCER
251 FDLHIRP  VQGGEL  NGDKA  HDAAV  FNRNA  EYWIR  RFP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLSLSCLHTLGNRLGHLAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDTETMFKAVHGWHEHVQQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFFRKPEDTETMFKAVHGWHEHVQQALDKHEG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGRYISQQLPPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSTIQQ					
g505	LLFITPHIGSYDLGGRYISQQLPPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSTIQQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKVTLLFF					
g505	VKQIIKALRSGEATIVLPDHPVSPQEGGEGVWVDFFGKPAYTMTLAAXLAHVKGKVTLLFF					
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLPGGQGFDLHIRPVQGGELNGDKAHDAAVFNRNAEYWIRRFPTHI					
g505	CCERLPGGQGFVLHIRPVQGGELNGDKAHDAAVFNRNTEYWIRRFPTQYLFMYNRYKTP					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1   ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAAGT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGTTG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTTC GCGGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1   MFRLLQFRLFP PLRTAMHILL TALLKCLSL PLSLHLTLGN RLGHlafYLL
51  KEDRARIIVAN MRQAGMNPDP KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAHVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFFLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLLQFRLFPPLRTAMHILLTALLKCLSLPLSLHLTLGNRLGHlafYLLKEDRARIIVAN					
a505	MFRLLQFRLFPPLRTAMHILLTALLKCLSLPLSLHLTLGNRLGHlafYLLKEDRARIIVAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAHVHGEHVQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAHVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYMTLAAXLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAVFNRNAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```
1 ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51 CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCGACCCC AAAACGGTCA AAGCCGTTT TCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCTT GCCCGACCAC
601 GTCCCTTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGA AAAC CCTGTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```
1 MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGH LAFYLL
51 KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGL ELAPA FFRKPED IET
101 MFKAVHGWEH VQQALDKHEG L LFITPHIGS YDLGG RYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTS IQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YTM TLAAKLA HVKG VKTLFF C CERLPGGQG
251 FDLHIRPVQG ELNGDKA HDA AVFN RNAEYW IRRFP TQYLF MYNRYKMP*
```

m505-1/g505 94.3% identity in 298 aa overlap

```
10 20 30 40 50 60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGH LAFYLLKEDRARIVAN
g505 MFRLQFRLFPPLRTAMHILLTALLKCLSL LSL SCLHTLGNRLGH LAFYLLKEDRARIVAN
10 20 30 40 50 60

70 80 90 100 110 120
m505-1.pep MRQAGLNPD PKTVKAVFAETAKGGL ELAPAF FRKPED IETMFKAVHGWEHVQQALDKHEG
g505 MRQAGLNPD TQTVKAVFAETAKGGL ELAPAF FRKPED IETMFKAVHGWEHVQQALDKGEG
70 80 90 100 110 120

130 140 150 160 170 180
m505-1.pep LLFITPHIGSYDLGG RYISQQLPFP L TAMYKPPKIKAIKIMQAGRVRGKGKTAPTS IQG
g505 LLFITPHIGSYDLGG RYISQQLPFP L TAMYKPPKIKAIKIMQAGRVRGKGKTAPTS IQG
130 140 150 160 170 180

190 200 210 220 230 240
m505-1.pep VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKG VKTLFF
g505 VKQIIKALRAGEATIILPDHVPSPQEGG-GVWADFFGKPAYTMTLAAKLAHVKG VKTLFF
190 200 210 220 230

250 260 270 280 290 299
m505-1.pep CCERLPGGQGF DLHIRPVQGE LN GDKAHDAAVFN RNAEYWI RRFPTQYLFMYNRYKMPX
g505 CCERLPGGQGF V LHIRPVQGE LN GNKAHDAAVFN RNTEYWI RRFPTQYLFMYNRYKTPX
240 250 260 270 280 290
```

m505-1/a505 99.7% identity in 298 aa overlap

```
10 20 30 40 50 60
m505-1.pep MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGH LAFYLLKEDRARIVAN
a505 MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGH LAFYLLKEDRARIVAN
10 20 30 40 50 60

70 80 90 100 110 120
```

m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPED	ETMFKAVHGWEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPED	ETMFKAVHGWEHVQQALDKHEG
	70 80 90 100 110 120	
m505-1.pep	LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIK	AIDKIMQAGRVRGKGKTAPTSTIQG
a505	LLFITPHIGSYDLGGRYISQQLPFPLTAMYKPPKIK	AIDKIMQAGRVRGKGKTAPTSTIQG
	130 140 150 160 170 180	
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDF	FGKPAYTMTLAAKLAHVKGVKTLFF
a505	VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDF	FGKPAYTMTLAAKLAHVKGVKTLFF
	190 200 210 220 230 240	
m505-1.pep	CCERLPGGGQFDLHIRPVQGELNGDKAHDAAVFN	RNAEYWIRRFPTQYLFMYNRYKMPX
a505	CCERLPGGGQFDLHIRPVQGELNGDKAHDAAVFN	RNAEYWIRRFPTQYLFMYNRYKMPX
	250 260 270 280 290 299	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCATC	GCCCATGGCT	GCGGCGGTGT
51	TGTCAAACAA	AGCCTGTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAAGGCG
101	CGCGGTTGGC	TGAAGTAGTC	GTCATCGTCT	TGGCGGTAGT	CCCAGTGTGC
151	CGCGTCGCCG	TTGATTTTCA	AAGGCGGTTT	GGCGAAGTCG	GGTTGTTGCT
201	GCCATTGGCC	GAAGCTGTTG	GGTTCGTAGT	GCGCGAGGCT	GCCGTAGTTG
251	CCGTCGGCGC	GGCCTTGTC	GTCGCGCTGG	TTGCTGTGAA	CAGGGCAACG
301	CGGACGATTG	ACGGGGATTT	GGCGGAAGTT	CACACCCAAG	CGGTAACGTT
351	GCGCGTCGGC	GTAATTGAAC	AAACGGGCTT	GCAACATTTT	ATCCGGGCTC
401	GCGCCGATAC	CGGGAACGAG	GTTGCTCGGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTTCG	GATTGCGGTT	CAACTCGAAT	TCGCCCCACTT
501	CAATCAGCGG	ATAGTCTTTT	TTCGGCCAAA	CTTGGTCAA	GTCAAACGGA
551	TGATAAGGCA	CTTTTTCGGC	ATCGGCTTCA	GGCATGACTT	GGATGTACAT
601	CGTCCATTTC	GGGAACTCGC	CGCGCTCGAT	GGCTTCGTAC	AGGTCGCGCT
651	GATGGCTTTC	GCGGTCGTCG	GCGATGATTT	TTGCAGCTTC	TTCGTTGGTC
701	AGGTTTTTAA	TCCCTTGCTG	GCTGCGGAAA	TGGAATTTCA	CCCAAAAACG
751	TTCGCCCCGCT	TCGTTCCAGA	AGCTGTAGGT	ATGCGAACCG	AAGCCGTGCA
801	TATGGCGGTA	GCTGGCGGGA	ATACCGCGGT	CGCTCATCAC	GATGGTAACT
851	TGGTGACAGG	CTTCGGGCAG	CAGCGTCCAG	AAGTCCAGT	TGTTTGTGGC
901	GGAACGCATA	TTGGTGCGCG	GATCGCGTTT	GACGGCTTTG	TTCAGGTCGG
951	GGAATTTGCG	CGGGTCGCGC	AGGAAGAACA	CGGGCGTGTT	GTTGCCGACC
1001	ACATCCAGT	TGCCTTCTTC	GGTATAGAAT	TTCAACGCAA	AACCGCGGAT
1051	GTCGCGTTCC	GCATCGGCTG	CGCCGCGCTC	GCCTGCCACG	GTGGTGAAAC
1101	GGGCGAACAT	CTCGGTTTTT	TTGCCGACTT	CGCTGAAAAT	TTTGGCGCGG
1151	GTGTATTGG	TGATGTCGTG	TGTTACGGTA	AACGTACCGA	ACGCGCCCGA
1201	ACCTTTGGCG	TGCATACGCG	GTTCCGGGAT	GACTTCGCGC	ACGAAGTCGG
1251	CGAGTTTTTC	ATTACGCCAC	AAATCTTGCG	TCAGCAGGGG	GCCGCGCGGG
1301	CCGGCGGTCA	GGCTGTTTTG	ATTGTCGGCA	ACGGGCGCGC	CGTTGTTTCAT
1351	GGTCAGATGG	GTTACGGGGC	ATTGGAGGT	AGTCATCGCT	CTTGTTCCCTT
1401	TTCTCAGGTT	GGTCAAATGG	GGGGCAAACG	GCTTACAGTA	CGATTGGCG
1451	GAAAGCGTAT	TCGTAACCGG	TTTCTTGATT	GTAATAAATT	TCTTGAATCG
1501	ACATTTTATT	TTCCTTTTGC	AAAACTATG	GATGCGATTA	TACGCCAAGA
1551	TTTTCGTTAT	TAA			

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

1	MAVFDEVGRI	AHGCCGVVKQ	SLFLRVVHQV	EQGARLAEV	VIVLAVVPVC
51	RVAVDFQRRF	GEVGLLLPLA	EAVGFVVRQA	AVVAVGAALS	VALVAVNRRAT
101	RTIDGDLAEV	HTQAVTLRVG	VIEQTGLQHF	IRARADTGNE	VARCEGGLFH
151	IGEEVFGLIAV	QLEFAHFNQR	IVFFRPNFGQ	VKRMIRHFFG	IGFRHDLVDH

201 RPFRELAALD GFVQVALMAF AVVGDDDFCSF FVGQVFNPLL AAEMEFHPKT
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAHH DGNLVQGFQ QRPEVPVVC
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH
 451 GQMGYGAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFAKTM DAIIRQDFRY *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
 51 TGCCGAACAA TGCCTGTTTC TCGCGTCGT TCATCAGGTT GAACAGGGCG
 101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTT GCGCAATCG GGTGTGTGCT
 201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG
 251 CCGTCGGCGC GGCCTTGCCC GTyGCGsTgr TTgCTGTgAA CAsGGCAACG
 301 CGGACGATTG ACGGGAATTT GCGGGAAGTT TACGCCCAA CGGTAGCGTT
 351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
 451 ATCGGCGAAG AAGTTTTCCG GATTGCGGTT CTCAAACGGA TGATAAGGTA
 501 CTTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC
 601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC AGGTTTTTAA
 651 TGCCTTGTTG GGTGCGGAAA TGGAAATTTCA CCCAAAAACG CTCGCTGCT
 701 TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA
 751 GCCGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT TGGTGCAGTG
 801 CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTGTGGC AGAGCGCATA
 851 TTGGTGCAGC GGTGCGGTTT GACGGCTTTG TTCAGGTCGG GGAACCTACG
 901 CGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC ACATCCCAGT
 951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTCT
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT
 1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCATACGGC
 1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT
 1151 CTTGTTCTT TTCTCAGGTT GGTCAAATGG GGTAAACGG CTTACAGTAC
 1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATTT
 1251 CTTGAATCGA CATTTTATTT CCCTTTTGTA AAAACTATGG ATGCGACTAT
 1301 ACGCCAAGAT TTTCGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHGV EQGARLAEIV VIVLAVVPVC
 51 RVAVDFORRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGNE VARCEGLLFH
 151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRYFFR VCFRHDLDVH
 201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFQ QRPEVPVVC
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQGTAD
 351 VAFICGAAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGKRTERAR
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVVH
 451 GQMGYRAFFG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES
 501 TFYFPFVKTM DATIRQDFRY *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFORRF					
	:: :: :: :: :: :: ::					
g506	MAVFDEVGRIAHGCGGVVKQSLFLRVVHQVEQGARLAEVVIVLAVVPVCRVAVDFORRF					
	10	20	30	40	50	60

750

	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAADVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFIRARADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAAFDGFXXVALMAFAVVGDDFGGFFVGVQVFNALL					
g506	VKRMIRHFFGIGFRHDLDVHRPFRELAALDGFVQVALMAFAVVGDDFCFFVGVQVFNPLL					
	190	200	210	220	230	240
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC					
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQCFGQQRPEVPVVC					
	250	260	270	280	290	300
m506.pep	RAHIGARVAFDGFVQVGEFARVAQEEHGRVVADHIPVAFFGKIFQGKTADVAFICGA					
g506	GTHIGARIAFDGFVQVGEFARVAQEEHGRVVADHIPVAFFGKIFQRTADVAFRICGA					
	310	320	330	340	350	360
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
m506.pep	IQPQILRQQAARTGGQAVLIVGNRRVAVHGMGYRAFGGSHRSCSFSQVGMGGKRLTV					
g506	IQPQILRQQAARAGGQAVLIVGNRAVAVHGMGYGAFGGSHRSCSFSQVGMGGKRLTV					
	430	440	450	460	470	480
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTMDATIRODFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTMDAIRQDFRY					
	490	500	510	520		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1379>:

a506.seq

```

1  ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT
51  TGCCGAACAA TGCCTGTTTC TGC CGTCGT TCATCAGGTT GAACAGGGCG
101 CGCGGTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGC GC
151 CGCGTCGCCG TTGATTTTCA AAGCGGTTTC GCGGAAGTCG GGCTGCTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CGTCGCGCGC GTCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGGTTC ACAGGGATTT GCGGGAAGTT CACGCCCAAG CGGTAGCGTT
351 GCGCGTCGCG GTAATTGAAC AAACGCGCCT GCAACATTTT ATCTGGGCTG
401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATACGCA CTTTTTCCGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGGCT

```

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTGG GGTGCGGAAA TGGAAATTCA CCCAAAAACG
751 CTCGCCGTCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACCCGGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTCT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCTTT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQQ EQGARLAEIV VIVLAVVPVR
51 RVAVDFFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDV
201 RPFRLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRKTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFGG XHRSCSFSQV GQXGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

```

          10      20      30      40      50      60
m506.pep  MAVFDEVGRVAHCGGGVAEQCLFLRVVHQQEQGARLAEIVVIVLAVVPVCRVAVDFFQRRF
          |||||
a506      MAVFDEVGRVAHCGGGVAEQCLFLRVVHQQEQGARLAEIVVIVLAVVPVRRVAVDFFQRRF
          10      20      30      40      50      60

          70      80      90      100     110     120
m506.pep  GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG
          |||||
a506      GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG
          70      80      90      100     110     120

          130     140     150     160     170     180
m506.pep  VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
          |||||
a506      VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m506.pep  VKRMIRYFFRVCFRHDLDVHRPFRKLAALDGFXXVALMAFAVVGDDFGGFFVGQVFNALL
          |||||
a506      VKRMIRHFFRIGFRHDLVDVHRPFRKLAALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL
          190     200     210     220     230     240

          250     260     270     280     290     300
m506.pep  GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC
          |||||
a506      GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC
          250     260     270     280     290     300

```

	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQV	GELTRVAQEEHGRV	VADHIPVAFFGIKFQ	GKTADVAF	CIGCAAF	
a506	RAHIGARVAFDGFVQV	GELTRVAQEEHGRV	VADHIPVAFFGIELQ	RKTADVAF	CIGCAAF	
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFAD	FAEDFGAGVFGDV	VRYGKRTERARTFG	VHTAFGDDFAHEV	GEFF	
a506	ACHGGETGEHLGFFAD	FAEDFGAGVFGDV	VRYGKRTERARTFG	VHTAFGDDFAHEV	GEFF	
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQORAARTGG	QAVLIVGNRRRAV	VHGMGYRAFGGSH	RSCSFSQVGOMGG	KRLTV	
a506	IQPQILRQORAARTGG	QAVLIVGNRRRAV	VHGMGYRAFGGXH	RSCSFSQVGQXG	GKRLTV	
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCN	KFLESTFYFPVKT	MDATIRQDFRYX			
a506	RFGGKRIRNRFLDCN	KFLESTFYFPVKT	MDATIRQDFRYX			
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```
1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTCAGACGG
101 CCTTTGCGCT CTTCGTGCTT GGCAACGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGAATTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTT CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCCGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTCGA TCGGTTGGTG CAGGTTTTGC CGGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```
1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL
51  LLLRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFPDLQLVF LKLHADLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```
1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTTAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTTCGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGAA GGCAGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTT TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTAAC TCGCCTGCGC TGCCTGCTTG
401 TCGCGTTCGA TCGGTTGGTG CAGGTTTTGC TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTG CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```
1  MLLLTLQQGG CFLRGGGFGF VGQVXGLVFL FQTFALFVL GNRLFGMGKL
```

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQGGGCFRLRGGGFGFVGVQVXGLVFLFQTTTFALFVLGNRLFIMGKLLLLLQRFQFAAD					
	: :					
a507	MLLLALQGGGSFLRGGGFGFVRQIQGLVFLFQTTTFALFVLGNLFGMGKLLLLLQRFQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

754

```

m507.pep    AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507        AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
             70      80      90      100     110     120

             130      140      150      160      170      180
m507.pep    LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
             |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507        LMDALHLRLRLLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
             130      140      150      160      170      180

m507.pep    VYFV VX
             |||||
a507        VYFV VX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGACG GGTTTGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTG ATCTGCGCGA GTTTTCTCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GGCGATTTCG TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRLGLQ GLYAGVLLPA LFLNLREFFL
51 HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEKLLPAF LPVQGLLFEP
101 GDLLPVVFLF RVEFVDGDFG KPVLA VG FQ GKRLRFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGACG GGTTTGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTG ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCAAGCTG
301 GGCGATTTCG TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAGGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRLGLQ GLHFSVLLPA LFLNLREFLL
51 HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEKLLLA F LPVEGLLFKL
101 GDLLPVVFLF LVEFVDGDFG KPVLA VG FQ GKRLRFOTAL LLLAAVRGGL
151 LLVFEFGGGF LQGNDDV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

755

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLLLQQGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
g508	MVAFGVDQGFLLLLQQGGLGGGLKLRQLGLQGLYAGVLLPALFLNLREFLLHGDVFFVQVRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFKLGDLLPVVLFLLVEFVDGDFG					
g508	YGFQQLVELDVLLVVLELGFIGEGKLLPAFLPVQGLLFEPGDLLPVVLFLLVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQGNDVV					
g508	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQSSDVV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTGTCAG GGTTCGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCTCTG
151 TACGACAATA TATTCTTCGT CCAACTCTG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGTT GTTCAAGCTG
301 GGCAATTTGC TGTGTTAGT TTTGTTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLLAFL LPIEGLLFKL
101 GNLLLVVLEL LVELVDGDFG KPVLA VG FQQ GKLRL FQTLL LLLAAVRGGL
151 LLVFEFGGGF LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLLLQQGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLLLQQGGLGGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFKLGDLLPVVLFLLVEFVDGDFG					
a508	YGFAQLFELDVLVLELGFIGEGKLLLAFLPIEGLLFKLGNNLLVVLFLLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQGNDVVX					
a508	KPVLA VG FQQGKLR L FQTALLLLAAVRGGLLLVFEFGGGFLQNGDVVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

```

1   atgggtcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcggttcag gctgttgtag
101 tcttccaagc ctgctgtgtg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgaggc cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgctga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttggggccgaa gcataaggct cgagaaagcc gaatttgtag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aaggttcttc ggtgcgggag atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggatggaaa
501 gcggcagttc gcggtaaagt ttgtcagatt cgctgcggtg aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaa cgcagggttt cggcagaaac
601 aaacggattg ccgtcgcggc cgccgccgat ccagccgccg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggtag ggcttcaaaa aagctcatcg ggaagatgga
751 cagcccgctg ttgatttcgt cgttgacgct gagtttgtag cggcgcgctt
801 cgctggtctg ccacaagccc agaagcacgg tgctgatttc gcggcgacgc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcggttgc gcagcagcg
901 gcggatgcgg cgggtgaaat tcaaaacggc ttggcgttgc acttcggtcg
951 ggtgcgcggc caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgctgtcgtc ggaagtggac aagagtttga
1251 ccgttttcgac aaccaacggc gaggttcttc cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgccgcc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgccg aaccgttcac actttaacca
1451 ctcatgtccc gaaatgccgt ctgaagttag acgccgcccg acggcgcgct
1501 tacaatcgcc cgcaactggt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctccctgctg ggtacagccg ccacatcttc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatac
1651 tttggtcgtc ggctgcggcg gattgggcgc cgccgccccct gccctatctc
1701 gccgcctcgg gggctggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1   MVAVCDERAV QRTLVQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVQCQAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVVD EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAAFALROQ
301 ADAAVEIQNG LALHFGRVRG QNGGNRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFOKFR VRRQSRVLR
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVTPKCR LKLNAARRRR
501 YNRPLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLLRRIGR RRPCIPSPR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1   ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTCGTTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTGT GAAAAGCTCG GCAACCACAT CGGCGTGTGT
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CCGTTGTCGA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCAGCGCG GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGGT AGGGTTCTTC GCGCGGGCGG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCAGATT CGCCGCGATA GAAGCGGAAC

```

```

551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601 AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751 CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTtC GCgGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901 GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTGC
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTGTC CGTCGGCTTT CCCCCTTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GGCGTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTAAATC GTGGGTTTGT TGTTCTGTTCA ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTTCT CTCTCGTCTG CCGTAAATAT
1401 TGTAAATGTA CCCCAAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTGTC TGCGGTACAG CCGCCACATC
1601 CTCTTGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTCTG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```

m509.pep
  1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
 51  ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101  LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151  VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201  KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251  HAVVDFVVD AEFVAARFAGL PQAQQDSVDF AAQPCQRVGI GAAAFALRQC
301  ADAAVEAXDG LALHFGVRVRL QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351  QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401  YFFNQCRVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451  VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNAAARRQ
501  RYNRPQLFFS EHHHDHDRTR QRRCI PAAVQ PPHPLGRNRH RRAAETFRR
551  YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

```

m509/g509
      10      20      30      40      50      60
m509.pep  MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509      MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH
          10      20      30      40      50      60

      70      80      90      100     110     120
m509.pep  HVKAEHGYGTDEVCQTAFGKQTAAVVDKGT LQFFQIIQKLLCRSIRLEKAEFAAHTQTER
          ||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509      HVEAEHGHGTDEVCQTAFGKQAAAVVDKGT LQFFQII EKFLGRSIRLEKAEFAAHTQTER
          70      80      90      100     110     120

      130     140     150     160     170     180
m509.pep  ARFAHSARHNVDGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g509      ARFAHSARHNVDGAAGVFFGAGDFFVREGQCCHYVVVDFAADGKRQFAVKFEFAAV
          130     140     150     160     170     180

```

a509.seq

BNSDOCID: <WO__9957280A2 | >

759

```

901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTGC
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCCTTTG AGCCTGCGGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGCG TTCTTCGTGG ATTTGGCGGC
1101 GGCCTTCGTG GTGCACGTCT TCGGCGATGT TCAAATCTG GCGAACAGG
1151 CCGCAGGCCA AGGTAAATC GTGGGTTTGT TGTTTCGTCCA ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTGT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACTTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCCTATCTC
1701 GCCGCTTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

```

a509.pep
1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGNGATVGFF GAGGFFVGRF
151 VGQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVAVAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKKAHRKDG
251 HAVVDFVVD AEFVAARFAGL PQAQDSDVDF AAQPCQRVGI GTAFALRQQR
301 ADAAVEIQDG LALHFGRVRG QNGGNRIVQ LPLHFAVGF PRFEPADGFR
351 QAAFRAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRGRFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNV PMPHPCQTVH TLTARVPKCR LKLNARRQR
501 YNRPQLFXSE HHHDHDRTRQ RRCIPAAVQP PHPLGRNWHR RAAETFRRAY
551 FGRRLRRFGC RXPCFISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH					
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVVFQACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIEKF LCRSIRLEKAEFAAHTQTER					
	70	80	90	100	110	120
m509.pep	ARFAHSARHNVGDGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
a509	ARFAHSARHNVGNGATVGFFGAGGFFVGRFVGQRHHIAVDFDAADGERQFAVEFVEFATV					
	130	140	150	160	170	180
m509.pep	EAEHGIGVAAEGKAQGFGGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ					
	190	200	210	220	230	240
m509.pep	GFEKAHREDGHAVVDFVVD AEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGTAFALRQQC					
a509	GFKKAHRKDGHAVVDFVVD AEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGTAFALRQQR					
	250	260	270	280	290	300
m509.pep	GFEKAHREDGHAVVDFVVD AEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGTAFALRQQC					
a509	GFKKAHRKDGHAVVDFVVD AEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGTAFALRQQR					
	310	320	330	340	350	360

```

m509.pep      ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRPFEPADGFRQAAFRAAASG
a509          ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFRPFEPADGFRQAAFRAAASG
              310      320      330      340      350      360

              370      380      390      400      410      420
m509.pep      FFVDLAAAFVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVVGSGQEFDCFD
a509          FFVDLAAAFVHVFGDVQNLGEQAAGQGXIIVGLLFVQLRQYFFNQCRVVGSGQEFDRFD
              370      380      390      400      410      420

              430      440      450      460      470      480
m509.pep      NQRRGFFVQVEVEQGLFQKFRVRQRSLVWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV
a509          NQRRGFFVQVEVEQGLFQKFRVRQRSLVWIVQNMQLHDFSLI-AVNTVNVPQMPHPCQTV
              430      440      450      460      470

              490      500      510      520      530      540
m509.pep      HTLTARVPKCRLKLNAAARRQRYNRPQLFFSEHHHDHDRTRQRRICIPAAVQPPHPLGRNRH
a509          HTLTARVPKCRLKLNAAARRQRYNRPQLFXSEHHHDHDRTRQRRICIPAAVQPPHPLGRNWH
              480      490      500      510      520      530

              550      560      570
m509.pep      RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
a509          RRAAETFRRAYFGRRLRRFGCRXPCPISPLFASARX
              540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1   atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaaagcg
51  ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggagggttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
201 gcggccgcct tcgcgatgg cttcggttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttggtc gatgttcac ctttaaatcct
351 tattgctgcg tttcctgccg ttggggagg cgcgtgcca gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1   MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1   ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTTATTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCGTTCA GGGAGGTTT CAACAGGTGCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTGCGCTTT GCCGTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 GCGGTGCAwG ACTTCsAtGT GGA CTGTGTTGATGTTTCATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG CCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1   MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
g510	MPSRTPQGKRGYSCPKRDSAFWQALSISVILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1   ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTTATTCCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTGCGCTTT GCCGTTGAGC ATTCGCACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 G. CGTGCATG ACTTCGATGT GGAATTGTTT GATGTTTCATC CTTTAATCCT
351 TATTGCTGCG TTCTCTGCCG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1   MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNR
51  WTTLSSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 XVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
a510	MPSRTPQGKRGYSCAKRDSAFWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1   atgaaagtgc ttgttttagg tgcgggtgtt gccggcgat cctccgtgtg

```

```

51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101  gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151  tataccacgc cttgggctgc acccggtatt ccgaccaaag cactgaaacg
201  gctgtttaa agccatccgc ctttactgtt ccgccctgac ggcggcctgt
251  atcaaatcga atggctgtgg cggatgctgc aaaactgcac ggcaacgcgc
301  tatcaaatca ataaagagcg catggtcagg atttccgaat acagccgtga
351  aatgttccgc cgttttgaag cgcaaaccga catgaatttt gagggacgca
401  aaaaaggagc gttgcagatt ttccgccaaa ccgaagaagt cgaagcggca
451  aaacaagaca ttgccgtttt ggaacgctac ggcgtgcccgt accgccgtct
501  gaagcccga gaatgcgcag aattcgagcc tgcgctggca cgcgttacccg
551  ccaaaattgt cggcggtctg cacctgcctg cggatgcgac cggcgactgc
601  cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtacg
651  gttctacttc aaccaaacca tcagccgcat cgaccacaac gggctgcgca
701  tcaaagccgt tgaacgaaa cagggcggtt tgaacagat gccgttgtct
751  gcgcgctcgg ctgcttcagc aggactgtgt tggcgagtt ggatctcaat
801  ctgcccatat atcccgtaa aggtatttcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

```

g512.pep
1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKRLFK SHPLLFRPD GGLYQIEWLW RMLQNCTATR
101  YQINKERMVR ISEYSREMFR RFEAQTDMNF EGRKKGTLQI FRQTEEEVAA
151  KQDIAVLERY GVPYRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201  RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251  ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

```

m512.seq (partial)
1  ..GTTTGGAAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAATTT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101  GCCTGCACCT GCCTGCAGAT GCGACCGCGC ACTggCGCCT CTTCACTGAA
151  AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTTCAACCA
201  AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAA ACCGTTGAAA
251  CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301  TCAGCAGGAC GGTTTTGGCG CAGTTGGATC TCAATCTGCC CATTATATCC
351  GTCAAAGGCT ATTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

```

m512.pep (partial)
1  ..VLERYGVPYR RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQEKV VRFHFNQNIS RIDHNLRIK TVETKQGGGLK QMPLSARSVA
101  SAGRFWRWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

```

m512/g512
m512.pep
10 20 30
VLERYGVPYRLKPEECAEFEPALARVTAK
g512
130 140 150 160 170 180
TDMNFEGRKKGTLQIFRQTEEEVAAKQDIAVLERYGVPYRLKPEECAEFEPALARVTAK

40 50 60 70 80 90
IAGGLHLPADATGDWRLFENLYKLCQEKGVRFHFNQNISRIDHNLRIKTVETKQGGGLK
g512
190 200 210 220 230 240
IVGGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQTISRIDHNLRIKAVETKQGGGLK

100 110 120
QMPLSARSVASAGRFWRWSWISICPFIPSKAIP
g512
QMPLSARSAASAGLCWRSWISICPFIPSKAIP

```


250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
  1 ATGAAAGTGC TTGTTT TAGG TGCTGGTGT GCCGGCGTAT CTTCCGCGTG
 51 GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAAACCAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCCTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATGCGCAG AATTCGAGCC TGCGCTGGCA CGCGTTACCG
551 CCAAAATTGC CGGCGGCGTG CACCTGCCCG CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTT AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAACGAAA CAGGCGGGT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
  1 MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
 51 YTPPWAAPGI PTKALKWLFK SHPPLLFPRD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMFV RFEAQTGMNF EGRKKGTLOI FRQTKEVEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVPYRRLKPEECAEFEPALARVTAK
a512      TGMNFEGRKKGTLOIFRQTKEVEAAKQDIAVLERYGVPYRRLKPEECAEFEPALARVTAK
           130      140      150      160      170      180

           40      50      60      70      80      90
m512.pep  IAGGLHLPADATGDWRLFTENLYKL CQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
           |||:|||||
a512      IAGGLHLPADATGDCRLFTENLYKL CQEKGVRFHFNQTISRIDHNGLRIKTVETKQGGLK
           190      200      210      220      230      240

           100      110      120
m512.pep  QMPLSARSVASAGRFWRWSWISICPFIPSKAIPX
           |||:|||||
a512      QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
           250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
  1 ATGGGTTC CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTGTCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTT GCGCGCGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTT GCGCGGTTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKMKG DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

m513.pep	10	20	30	40	50	60
	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
m513.pep	70	80	90	100	110	120
	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	130	140	150	160	170	180
	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRDYTAKLKMKGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	190					
	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

```
1 ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51 CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTACCAGT AACACGGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CCGCCCTGCC TACTACATCA CTCAGGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTTGTTCGC CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTCAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTAATCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTT CCGCGCGAAC GCGCGCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTG ATACCATCAT
951 CGTTTGTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTGAG CCGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGCGCT CCTCGCCGTC ATCCTGTTTA TGTTTGCCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAAGCCA TTGGCTGATT ACCGCGGTTT TCCGTATGCT GGTTTTGGCG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```
a513.pep
1 MNENFTEWLH GWVGAINDEP WSYLVYXLLG TGLFFTVTTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGGPGA
101 VFWMWVTALI GMSSAFVESH LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFLSL IFCFGVFEEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAGG LLGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILIYQ QPYGDLGAA LTQAAIVSQV
351 QQWAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WYFYGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*
```

m513/a513 100.0% identity in 191 aa overlap

```
m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513
260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
TIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY
|||||
a513
320 330 340 350 360 370
TIIIVCSCTAFIILIYQQPYGDLGSAALTQAAIVSQVQWAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL
|||||
a513
380 390 400 410 420 430
AYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMADMAMGIMAWINLVAILL

160 170 180 190
LSPLAFMLLRDYTEAKLMGKDPEFKLSEHPGLKRRIKSDVWX
|||||
```

a513

LSPLAFMLLRDY TAKLMGKDPEFKLSEHPGLKRRIKSDVWX
 440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq

```

1 atggttcaaa tacaggttgt gcgcgcgcgc gccgttgccc gtggtctgca
51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa
151 atagctgctg cggaaagagc gggggatgtg cggttcttcg cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggtggtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgg cgcaaagtgc gccggcgccg ggtttgaccg
401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtacca
451 tgctgcgcgc tgcattccgt tttcgtcggc ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgctttgc cgggtgtcgg caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc gggtttgcac gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttgcgattgt ttgccaagc
651 cgacggcgcc tccgtatccc aaatcccatt cgtggttaaag gtcggggctg
701 ccgatgtgtt gcgccatcaa ctccggggtc gcaagtccgg cgcaaccgtc
751 ttcggcggtg tggcgggcga tgcggcgccg gccgcggacg gtgtcgcgca
801 gggcttggtt ggagaagtcg gcggtgccgg cgcggccttt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgcct tgcgtgaact cgatttgcct
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcggc gccggtcgcg cccgctgctt ttgccaagtc gagcgtgcgg
1001 cggcagaggt cgaggagtcc ggaagcgggt tggttgaaca gcataacaat
1051 ctttcttggt ggagcgttgt ggcattttaa

```

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep

```

1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
51 IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECDEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFGV GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)

```

1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCCG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGCGG CGGGCGGCGG TTTGACCGAT GGTTTCGGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTGCGGTA AACGTATTGG
401 TAATGGCCCG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGGCTCATC
451 CTCGTTACAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTk
501 CCGTATCCAA ATCCCATTCT TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGCGC CAACCGTCTT CGGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGCTCTG CTGGAACGCG ATTTGTTsGA TTTsGCCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGCGGCG GCAGAGGTCTG
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTTGCGG CATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

```

1  .GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVGDFDG VLQFFGEVVG STGAFAFAD VNGNVQRLVL LELDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

                                10      20      30
m515.pep                      GKSGGCAFFA QVEEIGQDFS ADAVDQETALA
                                ::| | | | | | | | | | | | | | | |
g515      AEEIAFDNAV LNHEARRGGNTFRIKIAAERAGDVRF FAQVEEIGQDFFADAVDQETALA
              30      40      50      60      70      80

                                40      50      60      70      80      90
m515.pep      VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
              | | | | | | | | | | : | | | | | | | | | | | | | | | | |
g515      VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
              90      100     110     120     130     140

                                100     110     120     130     140     150
m515.pep      GGIVPVVALHAVFVGGNDAAGNAVVRALPVCGKTVGVAVNVLMAGLHRRAFGVFDALIL
              | | | | | | | | : | | | | | | | | | | | | | | | : | | | | | |
g515      GGIVPVVALHSVFVGGDDAAGNAVVRALPVCGKTVGVAVNVLVLSGLHRRAFGVFDAAVR
              150     160     170     180     190     200

                                160     170     180     190     200     210
m515.pep      VQGGGLFALFCQADGGXRIQIPFVVKVGVAADV FCHQTGIGKSGATVFGGVAGDVGDFDG
              | | | | | | | | | | | | | | | | : | | : | | | | | | | | | |
g515      VQRCLFALFCQADGGFRIQIPFVVKVGVAADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
              210     220     230     240     250     260

                                220     230     240     250     260     270
m515.pep      LQFFGEVVGSTGAFAFADVNGNVQRLV LLELDLXDXAQPHADALSQXFAEIGFGGGCAR
              | | : | | | | : | | | | | | | | | | : | | | | | : | | | | |
g515      AQGLFGEVVGAGAAFAFADVNGNVQRFV LLELDLDFQAQAHADALSERFAEVGFGGGRAR
              270     280     290     300     310     320

                                280     290     300
m515.pep      RFCQVERAAA EVEEFGSGVVEQHRNLSXXCFAAF
              | | | | | | | | | | | | | | | | : | |
g515      CFCQVERAAA EVEEFGSGVVEQHNNLSWWSVAF
              330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

```

a515.seq
1  ATGGTTCAAA TAAAGGTTGT GCGCGCCGCC GCGGTTGCC CTTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCGC

```

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```

551 TAAACGTATT GGTAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCAT TCGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCNNNNGC GGCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CACTTGTCC TGCTGAACT CGATTTGTTC
901 GATTCGCCC AGCCGCACGC TGACGCTTG TCCCAATGAT TCGCTGAAAT
951 CGGCTTCGGC GGCGGTTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAGAAAT
1051 CTTTCTTGAT GATGCTTTGC GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1422; ORF 515.a>:

```

a515.pep
1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEIEA  FDNVNLNHEA  RCGGNAFRIK
51  IAAERAGDV  RFFAQVEEIG  QDFFADAVDQ  ETALAVERSA  GECADVSDK
101 TARNGGIEED  GVVACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151 VVALHAVFVG  GNDAAGNAV  RALPVCCKTV  GVAVNVLVMA  GLHRRAFGVF
201 DALILVQGG  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251 FGGVAGDVXX  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RLVLKLDLF
301 DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAEVEEF  GSGVVEQHRN
351 LS**CFAAF*

```

m515/a515 92.1% identity in 304 aa overlap

```

m515.pep                                10      20      30
                                         GKSGGCAFFAQVEEIGQDFESADAVDQETALA
                                         ::| | | | | | | | | | | | | | | |
a515      AEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVIDQETALA
           30      40      50      60      70      80

m515.pep           40      50      60      70      80      90
VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
|||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
           90     100     110     120     130     140

m515.pep           100     110     120     130     140     150
GGIVPVVALHAVFVGNDAGNAVVRALPVCCKTVGVAVNVLVMAGLHRRAFGVFDALIL
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      GGIVPVVALHAVFVGNDAGNAVVRALPVCCKTVGVAVNVLVMAGLHRRAFGVFDALIL
           150     160     170     180     190     200

m515.pep           160     170     180     190     200     210
VQGGFLFALFCQADGGXRIQIPFVVKVGVDVFCQGTGIGKSGATVFGGVAGDVDDGGFDGV
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VQGGFLFALFCQADGGFRIQIPFVVKVGVDVLRHQLGVGKSGATVFGGVAGDVXXGADGV
           210     220     230     240     250     260

m515.pep           220     230     240     250     260     270
LQFFGEVVGSTGAFAFADVNGNVQRLVLLLELDLXDQAQPHADALSQXFAEIGFGGGCAR
| | : | | : | | : | | | | | | | | | | | | | | | | | | | | | | | |
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLFDFAQPHADALSQXFAEIGFGGGCAR
           270     280     290     300     310     320

m515.pep           280     290     300
RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
           330     340     350     360

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

g515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA

```

```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCGCGCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGTTTTCGG GGCTGTCCAT ATCCGATGCG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAGTGTCG GGTTTGCACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TGCCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTGCGGCA
801 GGGCTTGTTC GGAGAAGTCG GCGGTGCCGG CCGGCCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGTC TGCTGGAACG CGATTGTGTC
901 GATTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CGGCTTCGGC GCGGTCGCGC CCCGCTGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEEIA FDNVLNHEA RRGNTFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFLVLELDF
301 DFAQAHADAL SERFAEVGFG GGRARCFQVQ ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGTTTGT GCGCGCCGCC GCGGTTGCCG GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGATGCG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTCG CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAAATGGC GGTTCGACC GCCGCGCCTT CGGAGTTTTT
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGCG GGCTTTGACG GTGTCTTGCA
801 GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CCGGCCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGGAACG CGATTGTGTC
901 GATTTGCGCC AGCCGCACGC TGACGCTTGT TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEEIA FDNVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADSVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVSFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGG FALFCQADGG FRIQIPFVVK VGADVDFCHQ TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGFF GEVGSTGAFF AFADVNGNVQ RLVLLELDF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARAVTAEEIAFDNVLNHEARRGNTFRIKIAAAERAGDV
            |||
m515-1      MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNVLNHEARRCGGNAFRIKIAAAERAGDV
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
	190	200	210	220	230	240
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVADVLRHQ					
m515-1	GVAVNVLVMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLFCHQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
g515-1.pep	LGVGKSGATVFGGVAGDVGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLELDLF					
m515-1	TGIGKSGATVFGGVAGDVGGFDGVLQGGFGEVGGSTGAFAFADVNGNVQRLVLELDLF					
	250	260	270	280	290	300
	310	320	330	340	350	360
g515-1.pep	DFAQAHADALSERFAEVFGGGRARCFQVERAAAEEVEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GCGCTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGATGTG CCGTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACCGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGCGGCG GGTGTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGG GGCACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CCGTGTGCGG CAAAACCGTA GGTGTGCGCG
551 TAAACGTATT GGTAAATGCC GGTGTGACCC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGCG TCCTGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCC
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CCGGCGCTT GCCTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGAAACT CGATTTGTTC
901 GATTCGCCCC AGCCGCACGC TGACGCTTGT TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNAVLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAGNAVV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNGGIEEDGVVACRDAAA					

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```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70      80      90      100     110     120

              130     140     150     160     170     180
a515-1.pep  AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130     140     150     160     170     180

              190     200     210     220     230     240
a515-1.pep  GVAVNVLVMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGADVLRHQ
              |||||
m515-1      GVAVNVLVMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGADVLRHQ
              190     200     210     220     230     240

              250     260     270     280     290     300
a515-1.pep  LGVGKSGATVFGGVAGDVGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              |:|||||
m515-1      TGIKSGATVFGGVAGDVGGDFGVLQGGFGEVVGSTGAFAFADVNGNVQRLVLELDF
              250     260     270     280     290     300

              310
a515-1.pep  DFAQPHADALSQX
              |||||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1   atgttggttc gtaaaacgac cgccgccggt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccgga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccc gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtccttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcggtcaaa
451 ctcgacaatc ggaccattta cagcgctgac gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagtg
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttgttga tattggatgc
651 ggccggccgc gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1   MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGCLCLRY DTGRPDDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1   ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGCGC CTTGGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAGAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTGCGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
 551 TGCTGCGCA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
 601 AAGCTGTTTG CAAATATCTT ATATACGCC CCCTTTTGA TACTGGATGC
 651 GCGGGCGCG GTACTGGCT TGCCTGCGG GGCTCTGGT GCGGTCGTGG
 701 ATGCCGCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep

1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
 51 VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGCLRLY DTDKPADIAK LKQLGFEAVK
 151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK					
	: : : : :					
g516	MLFRKTTAAVLAATLILNGCTMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
	: : : : :					
g516	GSLVMMGGKYWFAVNPEDSAKLTGILLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m516.pep	FSTEGCLRLYDTDKPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
	: : : : :					
g516	FSTGGLCLRYDTGRPDDIAKLKQLEFKAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
	130	140	150	160	170	180
	190	200	210	220	230	239
m516.pep	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
	: : : : :					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq

1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
 51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAGG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCG TCAATCCTGA AGATTCGCGC AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CCTGCGGTC AAACCTGAAT CGCCGCCAG
 351 CCAGAATTTT AGTACCGAAG GCCTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTCTGAAGT
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAG ATATTGCATA TACGCCACC ACGTTGATAC TGGATGCCGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

```

1 MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WVVNPNEDSA KLTGILKAGL DKQFQMVEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDDKDQIRAFGVVAEDNAQLEK
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDDKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWVVNPNEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           GSLVMMGGKYWVVNPNEDSAKLTGILKAGLDKQFQMVEPNPRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGCLRYDTPDKPADIACLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           FSTEGCLRYDTPDRPADIACLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
              120     130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
              180     190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1 atgcatcggg ttccagacgg cattggagtg tcagtcgtgt tctgccgatt
51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacc
151 tgcgtctttc aatccccgatt tgatgttttt gggcaggctg atttggctgg
201 tgcgcgggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaac
251 attttcattt gtccggcggt ggtgttttgc gcttcgtcga ggatgatgta
301 tgcgcgggtt agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
351 tcaggccctt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1 MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT
51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDPLFG
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACGTTGTGCA GTTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTGCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGCGGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCGATTTCAA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKR TKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : : :					
g517	FNQLGYTVKAHQVIEGIIKRTEVGVD FLGQVSGQEAQFLTGF DGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGCTCTCG
101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAAGAAC
251 ATTTTCATT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCAAGCC CATCAGGTCA
401 TAGAGGCGAT CATAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLQTF					

```

          130      140      150      160
m517.pép  FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a517      FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVGTGKTQFLAGFDGRPHX
          130      140      150      160

```

```
g518.seq
1  atgacgtttt  cggcggcaaa  gctcaacatt  tcggcactga  tgttgtgtct
51  ttcggcagga  atgaccgttt  tactttccgc  ttttttactg  ctccgaccgg
101 aaggcagcat  cttattcaac  cattttttca  gcataaatat  tctgaccoga
151 agagcggcat  ctccacgggc  aaccgtgttc  agactgcata  aggcggtacg
201 attccacaag  atgcgaaaaa  ccataagcaa  aatgcgtaga  aactacgcgg
251 tccgaattac  cgcgcctcct  cgggcggcaa  cgcttcatta  taacagattg
301 ccccttaaaa  aatcagaccc  tgcttttgtg  cgggagtctg  aaatttga
```

g518.pep
1 MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51 RAASPRATVF RLHQAVRFHK MPKTISKMR NYAVRITPPP RAATLHYNRL
101 PLKKSDPAFV AESEI*

```
m518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCa GCATAAATAT TCTGACCCGG
151 AGAGCGGCAT CTCACAGGCG AACCGTGTTc AGACGGCAtC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCGc TAGAAACTAC GCGCTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTc ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGc CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTt TGTGGCAGAG TCTGAAATTT
401 GA
```

m518.pep

1	MTFSAAKLNI	SARMLCLSAG	MTVLLSAFLI	LRPEGSILFN	HFFSINILTR
51	RAASPOATVF	RRHQARFARC	RTINKRRRNY	AVRITPPSXA	ATRHYNRLPS
101	AAGLVRRERR	RCAVILSNGR	KKSDPAFVAE	SEI*	

Homology with a predicted ORF from *N. gonorrhoeae*

```
m518/g518
```

m518.pep MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRRPEGSILFNHFFSINILTTRRAASFPQATVF
||||| :|||
g518 MTFSAAKLNISALMCLSLGAMTVLLSAFLLLRRPEGSILFNHFFSINILTTRRAASPRATVF
 10 20 30 40 50 60

```

              70          80          90          100          110
m518.pep    RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRRRRCVILSN
              | | | | | : | | | | | | | | | | | | | | | | | | | | |
g518         RLHQA VRFHKMPKTISKMRNRNYAVRITPPRAATLHYNRLPL-----
              70          80          90          100

```

```

120      130
m518.pep  GRKKSDPAFVAESEI
           |||||
g518      --KKSDPAFVAESEI
           110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTCAT GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 ..... AAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQA-RFARCTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCVILSNG					
	:					
a518	RRHQAVRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
	110					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccttg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcgcg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttcgcg cgcaagaaat
501 ctttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccct tcaaacccaa agcggggcgg atgcgggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

```

101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANAEAN
251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFSP EAKTAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

```

m519.seq (partial)
  1 ..TCCGTATCG GCGTATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTCTGCG CCGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

```

m519.pep (partial)
  1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
		150	160	170	180	190
						200
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEAIRQIAAALQTQGGADAV				
g519		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANAEANRQIAAALQTQSGADAV				
		210	220	230	240	250
						260
m519.pep		160	170	180	190	200
		NLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAGQYVTAFKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

```

a519.seq
  1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTAGACGT

```

```

201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

a519.pep

```

1  MEFFIILLAA VVVFGEKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GOREAEIQQS EGEAAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 99.5% identity in 199 aa overlap

```

m519.pep                                     10      20      30
                                         SVIGRMELDKTFEERDEINSTVVAALDEAA
a519      YFQVTDPKLSYGS SNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
           90      100     110     120     130     140

m519.pep          40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRS MQAQITAEREKRARIAESEGRKIEQINLASGOREAE
a519      GAWGVKVLRYEIKDLVPPQEILRS MQAQITAEREKRARIAESEGRKIEQINLASGOREAE
           150     160     170     180     190     200

m519.pep          100     110     120     130     140     150
IQQSEGEAAQAVNASNAEKIARINRAKGEAESLR LVAEANAIAIRQIAAALQTGGADAV
a519      IQQSEGEAAQAVNASNAEKIARINRAKGEAESLR LVAEANAIAIRQIAAALQTGGADAV
           210     220     230     240     250     260

m519.pep          160     170     180     190     200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
a519      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
           270     280     290     300     310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

g519-1.seq

```

1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTACGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

```


801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAPFN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGCTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTGAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCATGCGC TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
 751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
 51 IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAPFN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
	190	200	210	220	230	240
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR					

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240
              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300
              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGCTCTC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 CTGAAGGTTT TGCGTTATGA GATTAAGAC TTGGTTCCGC CGCAAGAAAT
501 CGTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGC AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFQFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 QQREAEIQQS EGAEQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFQFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFQFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60
              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120
              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAITAERE
              130     140     150     160     170     180
              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1.pep  LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANA EAI RQIAAALQTGGADAVNLKIAEQYVA AFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgctc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gttaataatg ccggcgatgg
101 atttaacctt gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt ttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcaaacagt tcgaacggat cttttgacaa gggcgggcca cgggccgatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgcccaa gcggcgaggaa atttctctg cgtgtccccg caacacggca
501 gccgcaccgc cgccgaccgt acctaacctt aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILIFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCCLP FSMAENTASL
101 AMPVPPNNST KTSTSLRANS SNGSFDKGG RADFGGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTCGGRk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTGc .CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTCCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1 MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPP RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520

      10      20      30      40      50      60
m520.pep  MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW
          |||||:|:||||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       MPALLSIRANALPFSRISERMKLLVPLIMPAMDILILFAAKPSRTALMIGIPPATAASNW
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

      70      80      90     100     110     120
m520.pep  TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520       TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

      70      80      90     100     110     120

      130     140     150     160     170     180
m520.pep  SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYNLKDR
          |||||:|:|:| |||||:|:| ||||| ||||| ||||| ||||| |||||
g520       SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

      130     140     150     160     170     180

      190
m520.pep  CLLASLCLLVSRKCKY
          ||||| ||||| ||||| |||||
g520       CLLASLCLLVSRKCKY
          ||||| ||||| ||||| |||||
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1 ATGCCTGCGC TTCTTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51 CATTTTCGGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTCTGT TGCCGTATTC GGCGAGCAGT TTTTGTGTTGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TGCGACCACT TCGAACGGAT CTTTGACAAA GGCTG. .CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTCCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCAATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1 MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRRALMIG
 51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

151 RAPS~~SDG~~KFP~~P~~ RCPAT~~RQ~~PY~~R~~ RRPYP~~N~~LK~~D~~R CLLAS~~L~~CLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMD	LILFAAKPSRRALMIGIPPATAASNW				
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMD	LILFAAKPSRRALMIGIPPATAASNW				
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFP	PRCXATRQPYRRRPYPNLKDR				
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFP	RCPATRQPYRRRPYPNLKDR				
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSR	LKCKYX				
a520	CLLASLCLLVSR	LKCKYX				
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCgAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCgTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVFPNNSTT TSTSLRATSS
101 NGSLTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGTTTGTG GGGCTTTTTC
351 TTTCACTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCSASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVFPNNSTT TSTSSRATSS

```

101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSLRATSSNGSLTKAADGQIWRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKRREISSALSRNTAAAPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSRNTAAVPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCTGTGC CGTATTTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCG GACCAGTTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTCCTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNWTMTFCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKRREISSALSRNTAAVPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSRNTAAVPPPTVPKPKRPMFTGFIIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTCAAG
51 CCCATTGGGT GCGAATGCGG CCAAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTTC

```

151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCCGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

g521n.pep

```

1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTD
51 PPIGNYSSER YILPQTPEPA PPSNNGGQAV KYKAPVKTVS KPAKSNTPPQ
101 QAPVNNRRS ILEAELSNER KALTEAQKML SQARLAKGGN INHQKINAL*
151 SNVLDROQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

m521.seq

```

1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAG
51 CCCATTGGGT GCGAATGCGG CCAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAsCAAG CCGTCCAAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCCCGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

m521.pep

```

1 MKSKLLLLILI NFSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
51 PPIGNYSSER YIPPQTPEPV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNSRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

m521/g521

	10	20	30	40	50	60
m521.pep	MKSKLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
g521	MKSKLPLILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNSRRSILETELSNE					
g521	YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTPP-QQAPVNNRRSILEAELSNE					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
g521	RKALTEAQKMLSQARLAKGGNINHQKINALXSNVLDROQNIQALQRELGRMX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

a521.seq

```

1 ATGAAATCAA AACTCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

```

```

51 CCCATTGGGT GCGAATGCGG CCAAAATCTA CACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCCAAAA GCTGCCTCTC AACCGATTTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACATC
201 CGAACCGACA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCCGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AAACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATCCAAGCAC TGCAAAGAGA
501 ATTGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI NFSLISSPLG ANAAKIYCT INGETVYTK PSKSCLSTD
51  PPIGNYSSER YIPPQTSEPT PPSNGGQAV KYKAPVKTVS KPAKSNTPPP
101 QQAPSNNRRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSVLDRQON IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER					
a521	MKSKLPLILINFSLISSPLGANAAKIYCTINGETVYTTKPSKSCLSTDLPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRRSILETELSNE					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROONIQUALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROONIQUALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc cgaaacacga aacgccgacg gaagagcagg ttgccgcgcg
51  caaaaaagca aaagccaaaa tccgcaccat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctcccaatg cgcgatgtcc
151 aaaccgcagg caaaacagaa aattgtcgag tcttgcataa aaaatattcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccg tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtc
351 acaagaacag cttgacctgc tcggcggcgc aaacgcgtt gaaactcgag
401 acaacaatg tctcgcgcat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAM
51  KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKCMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51  CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GCTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAAA ACGATTGCGG GGCCCGCGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```


787

301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCCG CCTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMS
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGKLGAQEQ					
	:					
a522	SCVKNIPFAEKWQNDLRARGLDSDNNTRLTVDYCKCMWEQPLDRLSEKQISSFGKLGAQEQ					
	70	80	90	100	110	120

g523.seq

1	atgactgtat	ggtttgttgc	cgctgttgcc	gtcttaatca	tccaattatt
51	gacgggaacg	gtttatcttt	tggttgtcag	cgcggtttg	gcgggttcgg
101	gcattgccta	cgggctgact	ggcagcacgc	ctgccgccgt	cttgaccgcc
151	gcactgcttt	ccgcgctggg	catttgggtc	gtacatgcca	aaaccgccgt
201	gggaaaagtt	gaaacggatt	catatcagga	tttgatacc	ggaaaatatg
251	ccgaaatcct	ccgatacaca	ggcggaaccc	gttcgaagt	ttttatcgc
301	ggtacgcact	ggcaggcgca	aaatacgggg	caggaaagtgt	ttgaaccggg
351	accgcgcgcc	ctcatcgctc	gcaaagaagg	taacctcttt	atcatcgcaa
401	acccttaa				

g523 . pep

1 MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

m523.seq (partial)

```

1      .GCCGCTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51     nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGCGAGTA
101    CGCTGCGCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTTnG
151    TTCGTACACG CCAAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201    GGATTTGGAT GCCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251    ACCGTTACGA AGTTTTtAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301    GGGCAAGAAG AGCTTTtAAC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
351    AGGCAACCTT CTtATTATCA CACACCCTTAA

```

m523.pep (partial)

```

1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RGTWHAQONT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m523/g523

```

                                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVS AALAGSGIAYGLTGSTPAAVLT XALLSALGIXF
                |||||
g523      MTVWFVA AVLIIELLTGTVYLLVVS AALAGSGIAYGLTGSTPAAVLT AALLSALGIWF
                10      20      30      40      50      60

                                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDL DAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEEL EPGTRA
                ||||| : : : : |||||
g523      VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEV FEPGTRA
                70      80      90      100     110     120

                                120
m523.pep      LIVRKEGNLLIITHP
                ||||| : : |

```

g523

LIVRKEGNLLIIANPX

130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
  1  ATGACTGTAT  GGTTTGTGTC  CGCTGTTGCC  GTCTTAATCA  TCGAATTATT
 51  GACGGGAACG  GTTTATCTTT  TGGTTGTCAG  CGCGGCTTTG  GCGGGTTCGG
101  GCATTGCTTA  CGGGCTGACC  GGCAGCACGC  CTGCCGCCGT  CTTGACCGCC
151  GCTCTGCTTT  CCGCGCTGGG  TATTTGGTTC  GTACACGCCA  AAACCGCCGT
201  GGGAAAAGTT  GAAACGGATT  CATATCAGGA  TTTGGATGCC  GGGCAATATG
251  CCGAAATCCT  CCGGCACGCA  GCGGCAACC  GTTACGAAGT  TTTTATCGC
301  GGTACGCACT  GGCAGGCTCA  AAATACGGGG  CAAGAAGAGC  TTGAACCAGG
351  AACGCGCGCC  CTAATCGTCC  GCAAGGAAG  CAACCTTCTT  ATCATCGCAA
401  AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
  1  MTVWFVAAVA  VLIIELLTGT  VYLLVVSAA  LAGSGIAYGL  TGSTPAAVLT  AALLSALGI  X
 51  ALLSALGIWF  VHAKTAVGKV  ETDSYQDL  DAQYAEILRH  AAGNRYEVF  YRGTHWQA  Q
101  GTHWQAQNTG  QEELEPGTRA  LIVRKEGN  LLIIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

```

              10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLT XALLSALGIXF
              |||
a523           MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLT AALLSALGIWF
              10      20      30      40      50      60

              60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDL DAGQYVEILRH TGGNRYEVF YRGTHWQAQNTG QEELEPGTRA
              |||
a523           VHAKTAVGKVETDSYQDL DAGQYAEILRH AGGNRYEVF YRGTHWQAQNTG QEELEPGTRA
              70      80      90      100     110     120

              120
m523.pep      LIVRKEGNLLIITHPX
              |||
a523           LIVRKEGNLLIIAKPX
              130
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
  1  atgaagtacg  tccggttatt  tttcctcggc  acggcactcg  ccggcactca
 51  agcggcggt  gccgaaatgg  ttcaaatacg  aggcggcagc  taccgcccgc
101  tttatctgaa  aaaagatacc  ggcttgatta  aagtcaaacc  gttcaaactg
151  gataaatatc  ccgttaccaa  tgccgagttt  gccgaatttg  tcaacagcca
201  cccccaatgg  caaaaaggca  ggatcggttc  caaacaggca  gaaccgcgtt
251  acctgaagca  ttggatgaaa  aacggcagcc  gcagctatgc  gccgaaggcg
301  ggcgaattga  aacagccggt  taccaatatt  tcctggtttg  ccgccaacgc
351  ctattgcgcc  gcacaaggca  aacgcctgcc  gaccatcgac  gaatgggaat
401  ttgccggact  tgcttcgcc  acgcagaaaa  aacggctcaa  acgaaccggg
451  ctacaaccgc  actattctcg  attggtatgc  cgacggcgga  cggaaaggcc
501  tgcacgatgt  cggcaaagca  ccgcccgaac  tactggggtg  tttatgatat
551  gcacgggctg  a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
  1  MKYVRLFFLG  TALAGTQAAA  AEMVQIEGGS  YRPLYLKKDT  GLIKVKPFKL
 51  DKYPVTNAEF  AEFVNSHPQW  QKGRIGSKQA  EPAYLKHWMK  NGSRSYAPKA
101  GELKQPVTNI  SWFAANAYCA  AQGKRLPTID  EWEFAGLASA  TQKKRLKRTR
151  LQPHYSRLVC  RRRTERPARC  RQSTARTTGV  FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

```
m525.seq
1 ATGAAGTATG TCCGGTTATT TTWCTCTCGGC GCGGCACTCG cCrCACTCA
51 ArCGGCGGCT GcCGAAATGG TTCAAATCTGA AGGCGGCAGc TACCGCCCCrC
101 TTTATCTGAA AaAGATATAC GGCCTAGTA AAGTCAAACC GTTCAAAGCT
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCGCAATTG TCAACACTGA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGTC GCAGCTATTg GCCGAAGgCG
301 GgCGAATTAA AACAACCGGT AACCAATGTT TCCTGGwTTG CGCCCAAcGC
351 CTATGCGCC GCACAAGGCA AACGCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGA CTGCTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A
```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525.pep

1	<u>MKYVRLFXLG</u>	<u>AALAXTQXAA</u>	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL
51	DKYPVTNAEF	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHWMK	NGSRSYAPKA
101	GELKQPVNTV	SWXAAAYCA	AQGKRLPTID	EWEFAGLASA	TQXRLKRTR
151	LOPHYSRLVC	RRRTERPARC	RXKAARTTGA	FMICTG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

m525/q525

		10	20	30	40	50	60
m525.pep		MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLK	DTGLIKVKPFKLDKYPVTNAEF				
			:				
g525		MKYVRLFFLGTALAGTQAAAAEMVQIEGGSYRPLYLK	DTGLIKVKPFKLDKYPVTNAEF				
		10	20	30	40	50	60
		70	80	90	100	110	120
m525.pep		AEFVNSHPQWQKGRIGSKQAE	PAYLKHWMKNGSR	SYAPKAGELKQPV	TNVS	SWXAANAYCA	
					:		
g525		AEFVNSHPQWQKGRIGSKQAE	PAYLKHWMKNGSR	SYAPKAGELKQPV	TNIS	WFAANAYCA	
		70	80	90	100	110	120
		130	140	150	160	170	180
m525.pep		AQGKRLPTIDWEFAGLASATQ	KRLKRTLQPHYSRLV	CRRRTERPARC	RXKAARTTGA		
					:		:
g525		AQGKRLPTIDWEFAGLASATQ	KRLKRTLQPHYSRLV	CRRRTERPARC	RQSTARTTGV		
		130	140	150	160	170	180
m525.pep		FMICTGX					
g525		FMICTGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

```

a525.seq
1  ATGAAGTTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51  AGCGGCAGTG GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCTGATTA AAGTCAAAAC GTTCAAACATG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT CGCGAATTTG TCAACAGGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCG GCAGCTATGC GCCGAAGGCG
301 GGCGATTATA AACAAACCGT AACCAATGTT TCCTGGTTTC GCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACCGCTGCC GACCATTGAC CAATGGGAAT
401 TTGCCGGACT TGCCTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
1  MKFTRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFFKLDKYPVTNAEF
          ||::||: | |||| | | ||||| ||||| ||||| ||||| ||||| |||||
a525      MKFTRLLFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFFKLDKYPVTNAEF
          10      20      30      40      50      60

      70      80      90      100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
          70      80      90      100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA
          130     140     150     160     170     180

m525.pep  FMICTGX
          |||||
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
1  ATGAAGTACG TCCGGTTATT TTTCTCGGC ACGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACC CGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAGGCCCT
501 GCACGATGTC GGCAAGACC GCCGAACCTA CTGGGGTGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAACATG CCGCTTCCT CCGTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKGLHDV GKDRPNYGVG YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
1  ATGAAGTATG TCCGGTTATT TTTCTCGGC GCGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

```
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGGCC ACGCAGAAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```
1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51 DKYVPTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVNTV SWFAANAYCA AOGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*
```

m525-1/g525-1

97.6% identity in 251 aa overlap

```
10 20 30 40 50 60
m525-1.pep MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL DKYVPTNAEF
          |||
g525-1      MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL DKYVPTNAEF
          |||
10 20 30 40 50 60
m525-1.pep AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVNTV SWFAANAYCA
          |||
g525-1      AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA GELKQPVNTI SWFAANAYCA
          |||
70 80 90 100 110 120
m525-1.pep AOGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG
          |||
g525-1      AOGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKDRPNYWG
          |||
130 140 150 160 170 180
m525-1.pep YDMHGLIEWE TEDFNSSLLSSG NANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV
          |||
g525-1      YDMHGLIEWE TEDFNSSLLSSG NANAQMFC SGASVGSADS SNYAAFLRYG IRTSLQSKYV
          |||
190 200 210 220 230 240
m525-1.pep LHNLGFRCTSRX
          |||
g525-1      LHNLGFRCTSRX
          |||
250
m525-1.pep LHNLGFRCTSRX
          |||
g525-1      LHNLGFRCTSRX
          |||
250
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```
1 ATGAAGTTA CCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGATTTAA AACACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGGCC ACGCAGAAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAATA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLFC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK  NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA  TQKNGSNEPG
151 YNRTILDWYA DGDRLDLDV  GKGRPNYWG  YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF					
a525-1	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVNTVSWFAANAYCA					
a525-1	:					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWG					
a525-1						
	130	140	150	160	170	180
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWETEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV					
a525-1						
	190	200	210	220	230	240
	250					
m525-1.pep	LHNLGFRCTSRX					
a525-1						
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggttttac cagtctcctt ttttcagcct gtccagttgg cggcggtcgc
51  gcttggtcgg tctgccgtcg ggatgggagg aagtgatgcg gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgcctcgg gtgccgggag gcgttggttg ttcaaacctt
201 taaccttgat tttatgggga aggggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggtttact gtttttgact ttcgagccgt ttacttgaa
301 cctaccagct tcgatatgct tttgcgcaag ggaacggggtc ttgaaaaaac
351 gtgccgcca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatat gattttggtt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLVPSFFQP VQLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFF
51  IQKPRLCRA ALVVQTFNLD FMGKGIERQV DNIADVGFET VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIIEVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTCCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCCTTGGTGG TTCAAACCTT

```

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201 TAACCKTGAT TTTATAGGGA AGGG.AATTk AgCkTCaGty GrTwATaTCG
 251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTGTGTTT GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

m527.pep
 1 MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVL
 51 IQKPRXGCRA ALVVQTFNND FIGKXNXASV XXIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

m527.pep	10	20	30	40	50	60
	MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA					
g527	MVLPVSFFQPVQLAAVALGRSAVGMGGSDAAELVELFALFPQCCRFRVFFIQKPRLGCR					
	10	20	30	40	50	60
m527.pep	70	80	90	100	110	120
	ALVVQTFNNDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
g527	ALVVQTFNLDNFMGKIERQVDNIADVYGFTVFDLRAVYLNPTQFDMLLRKGTGLEKTCRP					
	70	80	90	100	110	120
m527.pep	130	140	150			
	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
g527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

a527.seq
 1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTGCG
 51 GCTTGGTTCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
 101 TCGAGCTGTT TCGCCTCTTC CCTCAATGTT GCCGTTTTCG CGTCTCTTTC
 151 ATACAGAAGC CGCGCCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
 201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
 251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
 301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
 351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
 401 TCTTTCATAC GATTTTGTGTT GAAATAATTG AATTGTGTTT GAGTTTAGCA
 451 TAA

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

a527.pep
 1 MVLPVSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVL
 51 IQKPRLGCR ALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN
 101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
 151 *

m527/a527 93.3% identity in 150 aa overlap

m527.pep	10	20	30	40	50	60
	MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA					
a527	MVLPVSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRFRVLFIQKPRLGCR					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m527.pep	ALVVQTFNXXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1   atggaaattc gggtaataaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcgggggt gtatgagtgt ttgtccttgt
101 cccgctggtg taagccgaga aaacctgccg ccatcgattt ttgggatatt
151 ggcggcgaga gtccgctgtc tttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatctt
251 acttttatag gaaaataggg aagtttgaag cctgcggggt ggattggcgt
301 acgcgtgacg gcaaaccttt ggttgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1   MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTTGGGATATT
151 GGCggcgaga GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1   MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEXCGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE					
	70	80	90	100	110	120

```

m528.pep      K
               |
g528          KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

```

               10      20      30      40      50      60
m528.pep      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
               |||||
a528           MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLED
               10      20      30      40      50      60

               70      80      90      100     110     120
m528.pep      YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
               |||||
a528           YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK
               70      80      90      100     110     120

m528.pep      K
               |
a528          KQGLRRNGLSERVRWX
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1  ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCTTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAA AAGCAGGGGT TCGCGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```

```

51 TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTGA
351 CTGCTTGGAA AAGCAGGGGT TGC GCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51 GGESPPSLGD YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

          10      20      30      40      50      60
g528-1.pep MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90     100     110     120
g528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90     100     110     120

          130
g528-1.pep KQGLRRNGLSERVRWX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1 ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51 TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT
151 GCGGCGGAGA GTCCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CCGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA
351 TTGTTTGAAG AAGCAGGGGT TGC GCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFCLK KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

          10      20      30      40      50      60
a528-1.pep MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          10      20      30      40      50      60

          70      80      90     100     110     120
a528-1.pep YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFCLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
          70      80      90     100     110     120

          130
a528-1.pep KQGLRRNGLSERVRWX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m528-1      KQGLRRNGLSERVRWX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
  1 atgaccata tcaaaccgt cattgccgcg ctgcactca tcgggcttgc
  51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
 101 ggtcgacccg cctgatcaaa ctccaagtcc cgctgattt gaacaacccc
 151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
 201 cggggatttg gaaaaacgcc gcacaccgcg cgtccaacag ccagcggatg
 251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
 301 gccaacgcct ggcttgcgt tgacggcaaa tccccgcgcg aaatctccgc
 351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
  51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
 101 ANAWLVVDGK SPAEISAAP..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
  1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
  51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
 101 GGTGCGACCG CCTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
 151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCCGGCG CCGTCCGCGC
 201 CAGCGATTTC GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
 251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
 301 CAACGCTGGC TCGTTGTCTGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
 351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
 401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
 451 CCCCAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
 501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
 551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
 601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
 651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
 701 TTGACGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
 751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTGG
 801 CGACTACGGC AGAAACTGGC GGCACACCGT GCTGCCCTC GACCGCATCG
 851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGTTCAA
 901 AAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
 951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCTG
1051 CTAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAACCT CATTCCGAAC TGCCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
  1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
  51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAENVLSV KGVRLERDGS
 101 QRWLVVDGKS PAEIWPLLKA FWQENGFDIK SEEPALIGME TEWAENRAKI
 151 PQDSLRLRLFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
 201 YGGKDKDTTV WQPSPPDPNL EAAFLTRFMQ YLGVGQQAE NASAKKPTLP
 251 AANEMARIEG KSLIVFGDYG RNWRTVLAL DRIGLTVVGQ NTERHAFLVQ
 301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
 351 LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

              10      20      30      40      50      60
g529.pep      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
```

```

a529.seq
1  ATGACCCATA  TCAAACCCGT  CATTGCCGCG  CTCGCACTCA  TCGGGCTTGC
51  CGCCTGCTCC  GGCAGCAAAA  CCGAACAGCG  CAAGCTCGAG  TACCAAAGCC
101 GGTGCGACCG  CCTGATCAAA  CTCGAAGTCC  CACCTGATTT  GAACAACCCC
151 GACCAAGGCA  ACCTCTACCG  CCTGCCTGCC  GGTTCGGGCG  CCGTCCGCGC
201 CAGCGATTTG  GAAAAACGCC  GCACACCCGC  CGTCCAACAG  CCTGCCGATG
251 CGAAGTATT  GAAAAGCGTC  AAAGGTGTCC  GCCTCGAGCG  CGACGGCAGC
301 CAACGCTGGC  TCGTTGTCTA  CGGCAAGTCT  CATGCCGAAA  TCTGGCCGCT
351 CCTGAAAGCC  TTTTGGCAGG  AAAACGGCTT  CGACATCAAA  TCCGAAAGAC
401 CCGCATCGG  ACAAATGGAA  ACCGAGTGGG  CGGAAAAACG  TGCCAAAATC
451 CCCCAAGACA  GCTTGCGCCG  CCTATTCGAC  ACAGTCGGTT  TGGGCGGCAT
501 CTACTCCACC  GGCAGCGCGC  ACAAATTCAT  CGTCCGTATC  GAACAGGGCA
551 AAAACGGCGT  TTCCGACATC  TTCTTCGCCC  ACAAAGCCAT  GAAAGAAGTG
601 TACGGCGGCA  AAGACAAGA  CACGACCCTA  TGGCAGCCCT  CCCCCTCCGA
651 TCCCAACCTC  GAGCGCGCTT  TCCTGACGCG  CTTTATGCAA  TATTTGGGCG
701 TTGACGGACA  GCAGGCGGAA  AACGCATCGG  CAAAAAAACC  TACCCTTCCC
751 GCCGCCACCG  AAATGGCGCG  TATCGAAGGC  AAAAGCCCTG  TTGTCTTTGG
801 CGACTACGGC  AGAAATTCGC  GGCGCACCGC  GCTCGCCCTC  GACCGCATCG
851 GGTAGACCGT  CGTGGGTCAA  AACACCGAAC  GCCACGCTTT  CCTGGTTCAA
901 AAAGCCCCGA  ACGAAAGCAA  TGCAGTTACC  GAACAAAAC  CCGGCCCTGT
951 CAAACGCCTG  CTGGGCAAAG  GCAAAGCGGA  GAAACCTGCC  GAACAGCCGG
1001 AACTGATTGT  CTATGCCGAG  CCTGTCCGCA  ACGGCTCGCG  CATCGTCTTG
1051 CTCACAAAG  ACGCGACGCG  ATATGCCGCG  AAAGACGCAT  CCGCATTATT
1101 GGGCAAATC  CATTCGGAAC  TGC GTTAA

```

a529.pep

1	<u>MTHIKPVIAA</u>	<u>LALIGLAACS</u>	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNPN
51	DQGNLYRLPA	GSgAVRASDL	EKRRTPAVQK	PADAEVLKSV	KGVRLERDGS
101	QRWLVDGKS	HAElWPLLKA	FWQENGFDIK	SEEPaIGQME	TEWAENRAKI
151	PQDSLRLRFD	TVGLGGYIST	GERDKFIVRI	EQKNGVSDI	FEAHKAMKEV
201	YGGKDKDTTV	WQPSpSDPNL	EAAFLTRFMQ	YLGVDGQQAE	NASAKKPTLP
251	AAENMARIEG	KSLIVFGDYG	RNWRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
301	KAPNESNAVT	EQKPGLFKRL	LKGKKA EKPA	EQPELIVYAE	PVANGSRIVL
351	LNKDGSAAYG	KDASALLGKL	HSER*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAELVLSVKGVRLERDGSQRWLVDGKSPAEIWPLLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAELVLSVKGVRLERDGSQRWLVDGKSHAEIWPLLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep    FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDKVGLGGIYSTGERDKFIVRI
a529        FWQENGFDIKSEEPaIGQMETEWaENRAKIPQDSLRRlFDTVGLGGIYSTGERDKFIVRI
            130      140      150      160      170      180

            190      200      210      220      230      240
m529.pep    EQGKNGVSDIFFaHKAMKEVYGGKDKDttVWQPSpSDPNLEaAFLTRFMQYlGVDGQQAe
a529        EQGKNGVSDIFFaHKAMKEVYGGKDKDttVWQPSpSDPNLEaAFLTRFMQYlGVDGQQAe
            190      200      210      220      230      240

            250      260      270      280      290      300
m529.pep    NASAKKPTLPaANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGlTVVGQNTeRHaFLVQ
a529        NASAKKPTLPaANEMARIEGKSLIVFGDYGRNWRRTALALDRIGlTVVGQNTeRHaFLVQ
            250      260      270      280      290      300

            310      320      330      340      350      360
m529.pep    KAPNESNAVTEQKpGLFKRLLGKGKAEKPAEQPElIVYAEPVANGSRIVLLNKDGSAYAG
a529        KAPNESNAVTEQKpGLFKRLLGKGKAEKPAEQPElIVYAEPVANGSRIVLLNKDGSAYAG
            310      320      330      340      350      360

            370
m529.pep    KDASALLGKLHSELRX
a529        KDASALLGKLHSELRX
            370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1   atgagtgcga gcgcggaat gacgggtttg atatgggtca tcgtgtcatc
51  ctgtgtgatg gatattaaag tgtttgcacat gttatgccgt ccgaacggtt
101 cagacggcat ggctatatat aaagtgtgcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgcccaa ggcgataacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1   MSASAAMTGL IWVIVSSCVm DIKVFVMLCR PNGSDGMAIF KVVLRlSGRR
51  GLLPVRLPSA ERAAGARAVER IRPRRIPIIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1   WTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTcATC
51  STGTGTGATG GATATTAAAG TGtYTGTTGC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTkTTGC WTGTCCGTTT yCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TGGGTTTCGC ATCTGCCCAg GCGGATACC GCCATTTCG GTGCGGCGGG
251 GCTGGGTTTC CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCTGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1   XSASAAMTGL IWVIVSSCVm DIKVXVAXCR PNGSDGMXIF KVVLRlSGRR
51  GLLXVRFPsa ERAAGGRAVR ICPGRIPPIIS VRRGWVRRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

```

m530/g530

m530.pep    XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRlSGRRGLLXVRFPsa    60
            |||

```

```
a530.seq
1  ATGAGTGC GA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTCA TC
51  CTGTGTGA TG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCATATATT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTGC CTGTCCGCCT TCCGTCAGCG GAACAGCGCG CAGGCGGCAG
201 TCGCGTTTCG ATCTGCCAG GCGGATACC GCCCATTCG TCGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTA AAT CGGAATCAGC CGGTCGTTGA
```

a530.pep

1	MSASAAMTGL	IWVIVSSCVM	DIKFVVALCR	PNGSDGMAIF	KVVLRLSGRR
51	GLLPVRLPSA	ERAAGGRAVR	ICPGRIPPIS	VRRGWVRRTW	CRKSESAGR*

```

      10      20      30      40      50      60
m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA
          |||||
a530      MSASAAMTGLIWVIVSSCVMDIKVFVLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA
          |||||
      10      20      30      40      50      60

      70      80      90     100
m530.pep  ERAAGGRAVRICPGRIPPISVRRGWVVRTWCRKSESVGRX
          |||||
a530      ERAAGGRAVRICPGRIPPISVRRGWVVRTWCRKSESAGR
          |||||
      70      80      90     100

```

g531.seq

```
1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCTTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
151 ATCTTG TGGA CGGTCGGACT CATCAGCCTT GGCGGCATAC TGGCGGACTA
201 TATGGCAGGC ATGTTGGGGG TAAAATACAC TGGGGCAGGC AAACTCGCCG
251 TCCGAGGTGC ATTGCGCCGG AGCATCATCG GCATATTTTT CTCCCTTCCC
301 GGACTAATAC TCGGCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
351 TCGGCCAAT ATGCTTCAGG CAGGTAAGC GGGCTTGGGT ACGCTGTTGG
401 GGCTTGTCGT CGGCACGGCG TTCAAATCG GTGCGCCCGT ATCCATCTTG
451 TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTTAA
```

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPGLAL</u>	<u>MFAGTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMA</u>	<u>MLGVKYTGAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	<u>LF</u>			

```
m531.seq
1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GGCGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCAT  GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
151 GTTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGGCATAC TGGCGGACTA
201 TGTGGCAGGC ATATGGGGGA CAAATATAC  CGGAGCGGGC AAGCTGCCC
251 TTCGCGCGC ATTGGCCGCG AGCATCATCG GCATATTTTT TCCTCTCCC
301 GGACTAATAC TCGGTCCCTT TATCGGCGCG GCGGCAGGCG AACTGATCGA
```

351 ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
 401 GGCTTGTCTG CCGCACGGCG TTCAAAATCG GCTGCGCnGT ATCCATCTTG
 451 TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1534; ORF 531>:

m531.pep

1 MTVLTVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
 51 VLWTVGLISL AGILADYVAG IWGKYTGAG KLAVRGALAG SIIGIFFSLP
 101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
 151 FILLVKYIAY LF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 531 shows 94.4% identity over a 162 aa overlap with a predicted ORF (ORF 531.ng) from *N. gonorrhoeae*:

m531/g531

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL					
	10	20	30	40	50	60
g531	MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGILWTVGLISL					
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN					
	70	80	90	100	110	120
g531	GGILADYVAGMLGVKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIDRRN					
	130	140	150	160		
m531.pep	MLQAGKAGLGTLGLVVGTA FKIGCAVSILFILLVKYIAYLF					
	130	140	150	160		
g531	MLQAGKAGLGTLGLVVGTA FKIGCAVSILFILLVKYIAYLF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1535>:

a531.seq

1 ATGACCGCCT TGCTCGTCAT CCTCGCCCTC GCCCTGATAG CCGCCGGTAC
 51 GGCGGGCATC GTTTACCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
 101 GAACCTGGCT GCTCGCCTAC TCCGGCGGCT ACCAAATCTA CGGCGCGGGC
 151 GTTTGTGGA CGGTCGGACT CATCAGCCTT GCCGGCATA TGGCGGACTA
 201 TGTGGCAGGC ATATGGGGGA CAAATATAC CGGAGCGGGC AAGCTCGCCG
 251 TTCGCGCGC ATTGGCCGCG AGCATCATCG GCATATTTT CTCCCTTCCC
 301 GGAATAATAC TCGGTCCTT TATCGGCGCG CGGCGAGGCG AACTGATCGA
 351 ACGGCGCAAT ATGCTTCAGG CAGGTAAAGC GGGCTTGGGT ACGCTGTTGG
 401 GGCTTATCGT CGGTACGGCG TTCAAAATCG GCTGCGCCGT ATCCATCTTG
 451 TTTATCCTGT TGGTGAAATA CATCGCCTAC CTGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1536; ORF 531.a>:

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFAGTWLLAY SGGYQIYGAG
 51 VLWTVGLISL AGILADYVAG IWGKYTGAG KLAVRGALAG SIIGIFFSLP
 101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
 151 FILLVKYIAY LF*

m531/a531 96.9% identity in 162 aa overlap

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL					
	10	20	30	40	50	60
a531	MTALLVILALALIAAGTAGIVYPALPGLALMFAGTWLLAYS SGGYQIYGAGVLWTVGLISL					
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN					

803

```

a531      |||||
          AGILADYVAGIWGTYKTGAGKLAVRGALAGSIIGIFFSLPGLILGPFIGAAAGELIERN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFKIGCAVSILFILLVKYIAYLFX
          |||||:|||||
a531      MLQAGKAGLGTLLGLVVGTAFKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acaggcggat tcgcctgatt tgggtgtacgg
51  ttggaagac aggccgccgt tcggaatgc gctcttgagc gcggttacct
101 atcttttggc gattttctgt ccgatgatta cccccgcgt gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgcgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CCGCCGCGCT GATTGTGGGC
151 GCGCGCTGGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGTTTGGC TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTTCGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCC GCGCGCGGCT CGGCGGAAG GCGGACGGCA
551 CGTTCGGCTC GATGAAAAAC TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTCGGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCGCGTACCG
751 TTTAAATACG GTTTTGCTTT CCACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG TGTTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTGGT CGCGGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTCGGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTG CGTTTGAGCC
1251 GGAAGTGTG AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTGCCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
 251 FKYGFADFVH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEYTKRL
 301 RGGLVADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
 351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
 401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
 451 EAAVKFDTDH LEH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKQADSPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	:	:				
m532	MSGQLGKGADAPDLVYGLED RPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGTLTKDAM					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1541>:

a532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAGGAT AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTCCGGTT GGGGATGCTG TCCATCCAGT CGGTGAATTT CTCGTTTCGTT
301 ACCGTCATGA TTGCGCTCGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTTCGACG TCTTGGGCGT ATCGTTTGTG GCGCGGTTT
401 TGGTGTGTTT TTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGTGTGGT GGTGATGCTG ATCGGCTTGA GTTTGGTACA
501 CGTCCGTATT ACCGATTTTC GCGGCGGCTT CGGCGCAAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAACAC TTGGGGCTGG CATCGCTGGT GCTGCTGATT
601 GTGCTGGTGT TCAATTGCAT GAAAAACCCG CTGCTGCGGA TGAGCGGCAT
651 TCGGTCGGT CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC GGCATGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTAAATATG GTTTTGCTTT TGACTGGCAC GCATTTATTG TGGCGGGTGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTG ACGCGGACGG
851 CAATGGTGTC CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCTTG
901 CGCGGCGGCG GTTGGCGGGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTCGCTG CCGCTGACGA CGTTTGACAA AAACAACGGC GTGATTACAG
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGA CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGG TTGATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGCCACG GCATCCGCAG GCGCGAAGCG
1201 GTAATTGCGG CAACGTCGGT CCGTTTGGGC TTGGGTGTGCG CGTTTGAGCC
1251 GGAAGTGTG AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1542; ORF 532.a>:

a532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

```

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVFV GAFLVCFSAW LPPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCKMNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFADFWDH AFIVAGAI FL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLED	10	20	30	40	50	60
a532	MSGQLGKGADAPDLVYGLED	10	20	30	40	50	60
m532.pep	AYLVSMAMVASGVGT	70	80	90	100	110	120
a532	AYLVSMAMVASGVGT	70	80	90	100	110	120
m532.pep	ISTLLGVSVFVGAFLVCFSAW	130	140	150	160	170	180
a532	ISTLLGVSVFVGAFLVCFSAW	130	140	150	160	170	180
m532.pep	ADGTFGSMENLGLASLVLL	190	200	210	220	230	240
a532	ADGTFGSMENLGLASLVLL	190	200	210	220	230	240
m532.pep	NLPLVTLVPVPFKYGFADFWDH	250	260	270	280	290	300
a532	NLPLVTLVPVPFKYGFADFWDH	250	260	270	280	290	300
m532.pep	RGGVLADGLVSVIATAGSL	310	320	330	340	350	360
a532	RGGVLADGLVSVIATAGSL	310	320	330	340	350	360
m532.pep	RAFTTIPSPVLGGAMVLMFGL	370	380	390	400	410	420
a532	RAFTTIPSPVLGGAMVLMFGL	370	380	390	400	410	420
m532.pep	KNLPVLFQNSISAGGITAVL	430	440	450	460		
a532	KNLPVLFQNSISAGGITAVL	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1 atgccctttc ccgttttcag acaantattt gcttngtcct tgctacggtt
51 ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatattaca tcgcttccaa tttcgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

```

351 catcgatgat tttgtcccgt tgtacggtgg tttggcgcggt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcggtt ctgtgccatg gtgatgtaga ggcgtttgcy ggcgcgggtg
551 atggcgacgt acatgaggcg gcgttcttct tccagggccg cgcgctcggc
601 aaggctcatt tgcgtgggga aacgcccctc ttccataccg gtgaggaaga
651 cggcgttgaa ttccaagcct ttggcggcgt ggacgggtcat cagttggacg
701 gcttttttcg ctgcccctgc ttggttttcg cgggattcga gggcggcggt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

```

g535.pep
  1 MPFPVFRQXF AXSLRFFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
 51 ACISNLHRFQ FRKLGIQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL PHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

```

m535.seq
  1 aTGCCCTTtC CCGTTTTTCAG ACGGCCTTTT GCTTTGTCTT TACTtACGTT
 51 TTTTGCCGTA AGTCAGATTTC TTGTATCCGA CATTTCACAC AGCGGTGTTT
101 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAACCTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTCGCCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTGG CGTGGCGGAC
301 GTTTTGTCCG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGT GCGGTAACTG
401 TCGTAGGCAG GCTTTTTGAC GGACAGGTAG TGCAATACTT CCGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCACGA
501 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTCGAGGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

```

m535.pep
  1 MPFPVFRFPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
 51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAFICGIDN HAGAEFGVAD
101 VLSDTETCVG LGLFVVVDFF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFFEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENGEGBV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

```

m535/g535
      10      20      30      40      50      59
m535.pep MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
      |||||: || ||| |||||: || ||||| |||||: ||||| |||||: ||||| ||
g535      MPFPVFRQXFAXSLRFFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ
      10      20      30      40      50      60

      60      70      80      90      100     110     119
m535.pep FRKLGVQLFHALFAEIDGQSGGFVAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVD
      |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: ||
g535      FRKLGIQFFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD
      70      80      90      100     110     120

```

807

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGR LFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHGLDFACAC						
	: : : : : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVEFQAFGGVDGHQLDGGFFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIXEGENGEGGVV						
	: : : :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1547>:

a535.seq (partial)

1	TTCAGACGGC	CTTTTGCCTT	GTCCTTGCTA	CAGTTTTTTTG	CCATAGGTCG
51	GATTCTCGAA	TCCGACATTT	CCAACAGCGG	TTTTTCGGAA	ACGATAGACG
101	CGTCAAATAT	TTTTGTCTGA	TACGAGTATC	CAGCCTGCAT	TCAAATTTTA
151	CATCGCTTCC	AATTTCGCAA	ACTTGGTGTC	CAACTCTTTC	ACGCCCTGTT
201	TGCCGAAATT	GATGGTCAGT	CGGGCGGATT	CGCCTTTATC	TGCGGCATCG
251	ATAATCACGC	CGGTGCCGAA	TTTGGCGTGG	CGGACGTTTT	GTCCGATACG
301	GAAACCTGCG	TAGGTTTGGG	GCTGTTTGTA	GTCGTCGATG	ATTTTGTCTT
351	TGGGCGCGGC	GGTTTGCGCG	GTGTTGCCAT	AGCGGTCGTA	GGCGGGTTTT
401	TTGACGGACA	GGTAGTGCAA	TACTTCGGGC	GGGATTTCTT	CGACGAAGCG
451	GGAGACGATG	CCGAATTGGG	TTTGTCCGTG	CAGCATGCGT	TGTTGCGCCA
501	TGGTGATGTA	GAGGCGTTTG	CGGGCGCGGG	TGATGGCGAC	GTACATCAGG
551	CGGCGTTCTT	CTTCGAGGCC	GCCGCGTTCG	GCAAGGCTCA	TTTCGCTGGG
601	GAAGCGGCCT	TCTTCCATGC	CGGTGAGGAA	TACGGCGTTA	AATCCAAGC
651	CTTTGGCGGC	GTGCACGGTC	ATGAGTTGTA	CGGCTTTTTC	GCCGCGCCT
701	GCTTGGTTTT	CGCCGGATTC	GAGAGCAGCA	TTGCTTAGGA	AAGCGAGGAT
751	GGGGAAGGCG	GGTCTGCTTG	A		

This corresponds to the amino acid sequence <SEQ ID 1548; ORF 535.a>:

a535.pep (partial)

1	FRRPFALSLL	QFFAIGRILE	SDISNSGFSE	TIDASNIFVG	YEYPACISNL
51	HRFQFRKLG	VLHALFAEI	DGQSGGFAFI	CGIDNHAGAE	FGVADVLSDT
101	ETCVGLGLF	VVDDFVFRG	GLARVAIAVV	GGFFDQVVQ	YFGRDFFDEA
151	GDDAELGLSV	QHALLRHGDV	EAFAGAGDGD	VHQAFFFEA	AAFGKAHFAG
201	EAAFFHAGEE	YGVKFQAFGG	VHGHELYGFF	ARACLVFAGF	ESSIA*ESED
251	GGGVV*				

m535/a535 88.7% identity in 256 aa overlap

	10	20	30	40	50	60
m535.pep	MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASNVFVGVEYPTYISNLHLFQF					
	: : :					
a535	FRRPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGVEYPTYISNLHLRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGFATFCGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
a535	RKLGVQLFHALFAEIDGQSGGFATFCGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVAVTVVGR LFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : : :					
a535	VFGRGGLARVAIAVVGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIIAXEGENGEggVVX					
a535	VFAGFESSIAXESEDGEggVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatacagg gacggcggcg atgcgctgca ctacctcaac
151 cgcataccga cacaatacgg ttgacacgcg ctggcacacg cgccggtttt
201 ggaaaaattcc gcccgacaggc acgcacgcta tctcacgctc aatcccgaa
251 acggacacgg cgaacaccat cccgacaatc cgactacac cgacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcaggtgcgg catttgtgcg
501 cgaaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaaatat
601 taccgaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcgc
701 tgccttattt ttacggggaa cgtcccgacc ccgtgccgga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgccggcaac gaccctaacg gcaggctgac cgcgcaccaa
901 ttcgcccttt tcccgtcaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgagg ttagaaaagg cgaaaaatat ttcattccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatat ctaccggcgg cagttcggca
1151 acagcctgtc cactaccgg caggaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagcgg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAAGVFIH TONQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RRQPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDVPPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQKGNEI RPVRVLTAGN DPNGLTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCG TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51  TTTCTACCAT ACCCAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAGAACTCC GCGCGCAGGC ACGCAAGCTA CTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRIQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNGVHENIS					
g537	LAHAPVLENSARRHARYLT LNPEDGHGEHH PDNPHYTAQK LTERTRLAGY LYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSD SDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSD SDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAA FVRENGKTVLVFNQGN					
	130	140	150	160	170	180
g537	GSFERACAKGRROPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGTTTTT
 201 GGAAATTC GCGCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGTGG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT
 651 GCGCGCACAG GAGCTGCTCT ATACAGCCTA TCCGTCGGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGCAATC CTGCCAGCAT TGATTTTCC GAGGCGGCAG GCAAAATTAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGTCA
 851 GGGTTTTTAA CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCAG AAAACCCGAT TACCCTTATT TTAGAGTAAA CGGCGGCGAG
 1051 ACACTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGCGCGGACG
 1101 CTGGTGTGTA GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTCAGCGTT
 1201 GACGGAATGG CGGGCAGCCG CATCAGCCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPPEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPGSRLSIGR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNIRIRAQIGLHK					
a537	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLNIRIRAQIGLHK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
a537	GRFERHCAQGRNQPEAGRKYRYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51 cgtcatgctg gtgggcgtaa tggttgataa agatgatacg ggcagcaatg
 101 ccgcccgtct gaacggtttt cagacggcat tggcggaagc cgtcgagctg
 151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaaccgca
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaagcagt tgccgcagac ggcattgatt tggtcgtatt caaccacgaa
 301 cttactccca cgcaggaacg caatttgga aaaatcctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat ttctgccgcg cgcgcccgca
 401 cgcaggaagg caggctgcaa gtcgagtgg cgcaattgag ccatttggcg
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggcg aaaccaaact ggaaaccgac cgccgattaa
 551 ccgcccacat gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagcgcgccc tgcgcgcgaa gtcccgcgag tcgggcagaa tcaaaacgtt
 651 tgcgctggtc ggctatacca atgtcgcaa atccagcctg ttcaaccggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc ggcggctgta catcagtccc gcatgcagca ttatcctgac
 801 cgataccgtc ggattcgtca gcgatctgcc gcacaaactg atttcgcctt
 851 ttcccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc
 901 gtcgatgctg ccgcccggaa cagcgggag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcac aaggtgtaca
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaatac

1	MSGRTGRNSA	TQAQPERVML	VGVMLDKDDT	GSNAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVAAD	GIDLUVFNHE
101	LTPTQERNLE	KILQCRVLDR	VGLILAIFAR	RARTQEGRLQ	VELAQLSHLA
151	GRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLTAHRINA	LKKQLANLKK
201	QRALARKSRE	SGRIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDQLFATLD
251	TTARRLYISP	ACSIILTDTV	GFVSDLPKHL	ISAFSTALEE	TVQADVLLHV
301	VDAAARNNSGQ	QIEDENVLQ	EIHAHDI PCI	KVYNKTDLLP	SEQNTGIWR
351	DAAGKIAAVR	ISVAENTGID	ALREAIAEYC	AAAPNTDETE	MP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

1	ATGACAGGCCA	GAACAGGCGG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGTAGTG
101	CCGCCCCTGT	GAACGGTTTT	CAGACGGCAT	TGCGCGAAGC	TGTCTGAGCTG
151	GTCAAAGCTG	CGGGCGGCGA	TTCGCTGCGC	GTGGAGACTG	CCAAACCGCGA
201	CGCAGCCGAC	ACCGCGCTGT	TGTCTGGCAC	GGGCAAGCGC	CGCGAGCTGT
251	CAGAAGCAGT	TGCCGCAGAC	GGCATCGATT	TGTCGTATT	CACCAACGAA
301	CTCACGCCCA	CGCAGGAACG	CAACCTTGAA	AAAGAACTsa	AATGCCGCGT
351	ATTGGACAGG	GTAGGGCTGA	TCTTGGCGAT	TTCGCTCGC	CGCGCCCGCA
401	CGCAGGAAGG	CAGGCTGCAA	GTCGAGTTGG	CGCAATTGAG	CCATTTGGCG
451	GGACCGTTGA	TACGCGTTTA	CGGCCATTGC	CAGAGCCAGC	CGCGCGGTAT
501	CGGCATGAAA	GGCCCCGGCG	AAACCAAAC	GGAAACCGAC	CGCGCATTTGA
551	TCGCCCATCG	GATCAATGCC	TTGATAAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCC	TGCGCCGCAA	GTCnCGCGAA	TCGGGCACAA	TCAAAACGTT
651	TGCGCTGGTC	GGCTATACAA	ATGTCGGAAA	ATCCAGCCTG	TCAACCGGC
701	TGACAAAGTC	GGGCATATAT	GCAAAGGACA	AGCTTAGTCC	CGAATGCAGC
751	ATTATCTCTG	CGGATACCGT	CGGATTCGTn	AGCGATCTGC	CGCAcAAACT
801	GATTTCCGCC	TTTTCTgCC .A	CGCTGGAAGA	AACCGCGCAA	CGCGATGTGC
851	TGCTGCACGT	CGTCGATGCC	GCCGCTCCGA	ACAGCGGACA	GCAGATTGAA
901	GACGTGGAAA	ACGTACTGCA	AGAAATCCAT	GCCGGCGATA	TTCCGTGCAT
951	cAAGGTGTAC	AACAAACCGC	ACCTGCTGCG	GTCTGAAGAA	CAAAACACGG
1001	GCATATGGCG	CGACGCTGCG	GGAAAAATTG	CCGCGCTCCG	CATTTCCGTT
1051	GCTGAAAATA	CCGGTATAGA	CGCACTGCGC	GGAAGCcATTG	CCGAGTCTTG
1101	TGCCGCCGCA	CCAAACACAG	ACGAAACCGA	AATGCCATGA	

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

1	MTGRTGGNGS	TQAQPERVML	VGVLMDKDG	GSSAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEAVAAD	GIDLVVFNHE
101	LTPTQERNLE	KELKCRVLDR	VGLILAIFAR	RARTQEGRLO	VELAQLSHLA
151	GRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLIAHRINA	LIKQLANLKK
201	QRALRRKSRE	SGTIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDKLSPECS
251	IILTDTVGVF	SDLPHKLISA	FSXTLEETAQ	ADVLLHVVD	AAPNSGQOIE
301	DVENVLQEIH	AGDIPCIKVY	NKTDLLEPSE	QNTGIWRDAA	GKIAAVRISV
351	AENTGIDALR	EAIAESCAAA	PNTDETEMP*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	:	:	:	:	:	:
g538	MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVFVNHELTPTQERNLEKELKCRVLDR					
g538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDLVFVNHELTPTQERNLEKILOCRVLDR					

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	70	80	90	100	110	120
m538.pep	130	140	150	160	170	180
	VGLILAI	FARRARTQ	EGRLQVELA	QLSHL	AGRLIRGY	HLQSQRGGIGMKGPGETKLETD
g538	VGLILAI	FARRARTQ	EGRLQVELA	QLSHL	AGRLIRGY	HLQSQRGGIGMKGPGETKLETD
	130	140	150	160	170	180
m538.pep	190	200	210	220	230	240
	RRLIAHR	INALIKQ	LANLKKQ	RALRRKS	RESGTIK	TFALVGYTNVGKSSLFNRLTKSGIY
g538	RRLTAHR	INALIKQ	LANLKKQ	RALRRKS	RESGRIK	TFALVGYTNVGKSSLFNRLTKSGIY
	190	200	210	220	230	240
m538.pep	250	260	270	280		
	AKDKL----	SPECSI	IILTD	TVGFVSD	LPHKLIS	AFSXTLEETAQADVLLHV
g538	AKDQLF	ATLDTT	ARRLYIS	PACSI	IILTD	TVGFVSDLPHKLISAFSATLEETVQADVLLHV
	250	260	270	280	290	300
m538.pep	290	300	310	320	330	340
	VDAAAPN	SGQOIE	DVENVLQ	EIHAGDI	PCIKVYN	KTDLLPSEEQNTGIWRDAAGKIAAVR
g538	VDAAARN	SGQOIE	DVENVLQ	EIHAGDI	PCIKVYN	KTDLLPSEEQNTGIWRDAAGKIAAVR
	310	320	330	340	350	360
m538.pep	350	360	370	380		
	ISVAENT	GIDALR	EIAIESC	AAAPNT	DETEMPX	
g538	ISVAENT	GIDALR	EIAEYCA	AAAPNT	DETEMPX	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1  ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCGTCTT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCGCCCCG CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTTGCGC
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAAC TGGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAACGTT
651 TGCCTGGTGC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GGCGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAAACTG ATTTCCGCCT
851 TTTCGCCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCGTCTCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTTG CTGAAAATAC
1101 CCGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1  MTGRTGRNGS TQAPPERVML VGVM LDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101 LTPTQERNLE KILQCRVLDR VGLILAI FAR RARTQEGRLQ VELAQLSLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

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201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPHKL ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
	: : : : :					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLD R					
	: : : : :					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRVLD R					
	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	: : : : :					
a538	VGLILAIFARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVG YTNVGKSSLFNRLTKSGIY					
	: : : : :					
a538	RRLIAHRINALKKQLANLKKQALRRKSRESGTIKTFALVG YTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLPHKLISAFSXTLEETAQADVLLHV					
	: : : : : :					
a538	AKDQLFATLDTTARRLYISPECSIILTDTVGFVSDLPHKLISAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	: : : : :					
a538	VDAAAPNSGQQIEDVENVLQEIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
	: : : : :					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgcgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagtcg ggcaacggca
101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
151 ttgcgcgtca tagggtgcgg cgggtgtagc tgtctgccg attttcaaca
201 gaatgtcgga gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggattgg
401 acttcgggca ggtcgtacag gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt ttttcgcgt cggcgggtcg tcgtttgtaa taactgccca
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggt cttcgccttc gtagcggacg gtcagatgca ggttttcggg
601 aacgtccagc ccgcagtggg aacaggtttt tttcatggca tttcggtttc

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651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtatatttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccgtgttt tgttcttcag acggcagcag
801 gtcggttttg ttgtacacct tgatgcacgg aatategttg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgt gttccgggcg
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtggcggaa aaggcggaaa tcagtttgtg cggcagatcg ctgacgaatc
1001 cgacgggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgccgtcg tgtcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccggttga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGFHK VGLDFGQVVQ ADLVEDFLGR
151 QFGFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPFLRA
301 AASTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAVMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTTTT TGTTGGCGG CTTCCGATTTT
151 TTGCGCGTCA TAGGGTGC GGTTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGac GCGGCaGcgG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGA CTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTTGG TCGAGGATTT CTGGGGCGG
451 CagCTCGGTT TTTTGC GCGT CCGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaAgG
551 GTTTCGCGGT CTTCGTTTTT GTAACGGACA GTCAGGTGGA GGTGTTTCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGGCA TTTCGGTTTT
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCCGCAGCGT CGCGCCATAT GCGCGTGT TTCTTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGC GCGG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CCGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTcAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLRVGGA LfVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVSVRI MLHSG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||
g539       MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

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	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539.pep	130	140	150	160	170	180
	LARAAGVGHKVGGLDFGQVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGVGHKVGGLDFGQVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539.pep	190	200	210	220	230	240
	GAQGFVAFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFQVGNQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSSTFSTSSICPLFGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSSTFSTSSICPLFRA					
	250	260	270	280	290	300
m539.pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRVAVSRVAKS					
	310	320	330	340	350	360
g539	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGCTGT TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAACACCGC CTCGCGCGTG CCGCGGTGGG TTTCCACAAA GTCGGAAGTG
401 ACTTCGGGCA GGTCTGACAG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTGCGCGT CGGCGGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GCGCGAGCAG
551 GTTTCGCGGT CTTCGTTTTT GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTTCATGGC TTTTCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTT
751 CCCGCAGCGT CGCGCCATAT GCCCGTGTTT TGTTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATT
851 CTTGCAGTAC GTTTTCCACG TCTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTCG CATATATGCC
1101 CGACTTGGTC AGCCGTTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF

```

51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAVRAVIEV DADDAVCTQK
 101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
 151 QLGFRLVGGA LFVITAQARV NNALCDCLTT GAAGFAVFVF VTDGQMVFVG
 201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
 251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
 301 AASTCSSTS AAVSSSSVAE KAEISLCGRS LTNPTVSVRI MLHSGLMYSR
 351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

m539/a539 97.1% identity in 345 aa overlap

m539.pep	10	20	30	40	50	60
	MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLAFFLVGGFDFLRVIGCGGVA					
a539	10	20	30	40	50	60
	MEDLQEIGFDVAAVKVGRQREHRLHHPQPGNGEADDVLAFFLVGGFDFLRVIGCGGVA					
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
a539	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
m539.pep	130	140	150	160	170	180
	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
a539	130	140	150	160	170	180
	LARAAGVFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDCLTT					
m539.pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFVGNITAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
a539	190	200	210	220	230	240
	GAAGFAVFVFTDQGMQVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISPAPWISCSTFSTSSICCPFLGA					
a539	250	260	270	280	290	300
	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISPAPWISCSTFSTSSICCPFLGA					
m539.pep	310	320	330	340		
	AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
a539	310	320	330	340	350	360
	AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSGLMYSRRRAVVSSVAKS					
a539						
	WSFAYMPDLVSRLNRLDLPTLVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq
 1 atgccgcct cccgacgcg caacgggggtg ttttatcaaa acggcaaaact
 51 tgccaatgcg gtttcgcgtt gccgattgcc aaaccggcaa acctttcccg
 101 tgccggtgcc gaaccgatg ccgtctgaac cttcagacg catcgggtgt
 151 ttatttgcc actcggacg gtgcaggttc gtattgtgtc gattcgtcgc
 201 cgtaatacag cacgccgagt ttgacgggga tgcgtccctg cgatttgccg
 251 tgggcgttg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
 301 gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccgccgc
 351 ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
 401 gcacggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep
 1 MPPSRRNGV FYQNGKLANA VSACRLPNRQ TFPVPVNPMP PSEPSDGIGC

51 L FVHSDGCRF V LCRFVAVIQ HAEFDGDASL RFAVGVGIAQ GIRAAAVFLL
 101 VEVFAFADFN HTRAAAFAP VEVPIGHIIV RRGTVSAVV DLRHIFPA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1569>:

m540.seq (partial)
 1 ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
 51 CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCGTC GCCGTAATAC
 101 AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
 151 GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
 201 TTTACGTTT GCTGATTTC AATCATGCGC CGCTGCCGCC GCCTTTGCGC
 251 CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
 301 TCCGCAGTCG TTGATTTCG CCATATTTT CCAGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1570; ORF 540>:

m540.pep (partial)
 1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEFDG DSAL*FAVGI
 51 GIPOGIGTTA IFLLEVFTE ADFNHARAAA AFAPVEIPIH HIIVRRGAV
 101 SAVVDLRHIF PA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 540 shows 85.7% identity over a 112 aa overlap with a predicted ORF (ORF 540.ng) from *N. gonorrhoeae*:

m540/g540

				10	20	30
m540.pep				PNMPSEPSD	GIGCLFVHPD	GGRFVLCRFV
g540	GNGV	FYQNG	KLAV	SA	CRLPN	RQTFFV
	10	20	30	40	50	60
	40	50	60	70	80	90
m540.pep	AVIQHAEFDG	DSALXFAV	GIGIPIQ	GIGTTAIF	LLVEVFTF	ADFNHARAAA
g540	AVIQHAEFDG	DASLRF	FAVGVGIA	QGIRAAAV	FLLVEVFA	FADFNHTRAAAF
	70	80	90	100	110	120
	100	110				
m540.pep	HIIVRRGAV	SAVVDLRHIF	PAX			
g540	HIIVRRGGT	VS	AVVDLRHIF	PAX		
	130	140				

L' estremita' N-terminale di meningococco e' assente perche' interviene la fine del contig

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1571>:

a540.seq
 1 ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAACT
 51 TGCCAATGCG GTTTCGATT GCAGATTGCC AAACCGGCAA ACCTTCCCG
 101 TGCCGATGCC GAACCGGATG CCGTCTGAAC CTTCAGACGG CATCGGGTGT
 151 TTATTTGTCC ACCCGGATGG GTGCAGGTTT GTATTGTGTC GATTCGTCGC
 201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTTCGGG
 251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
 301 GTAGAAAGTT TCACGTTTGC TGATTTCAT CACACGCGC CTGCCGCCG
 351 CTTTGCGCCA GTTGAAATCC CAATACACCA CATCATCGTA AGGCGCGCG
 401 GCGCGCGGC CGCAGTCGTT AATCTGGTTC ATGTTTTTCC A

This corresponds to the amino acid sequence <SEQ ID 1572; ORF 540.a>:

a540.pep (partial)
 1 MPSSRRNGV FYQNGKLANA VSDCRLPNRQ TFPVPMNPM PSEPSDGIGC
 51 LFVHPDGCRF V LCRFVAVIQ HAEFDGDASL *FAVGVGIPQ GIGTTAIFLL
 101 VEFTFADFN HTRAAAFAP VEIPIHHIIV RRGGAAGAVV NLVHVF

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVIFYQNGKLANAVSDCRLPNRQTFPVMFPNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
              10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHARAAAFAPVEIPIH
              |||||
a540      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHTRAAAFAPVEIPIH
              70      80      90      100     110     120

                                100     110
m540.pep      HIIIVRRGGAVSAVVDLRHIFPAX
              |||||
a540      HIIIVRRGGAAAVVNLVHVFP
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaaat ggtcgcgcat acggcggttg agcgctcctt cgctgatgtt
51 cagcgcggtt gtcagccggt tgacttggtg tgcgcgcgct tcgaacgcgg
101 cattcagggg gcggctgaag tcttcagacg gcatagcgtc tgcttcgcgc
151 gtttgccccg ccgcccgttc gatgcccgtt gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatgtt tcgccccaaat
251 gccccttttg gacggtttgc aggcaggatg ccgccaagcc gcgcagggtt
301 gggggcaaat cccatattct gaccggttcg cggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFVRRLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GGKSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTCGCGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGCGTCT GTCAGCCGCT TGACTTGGTG TGCGCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAATC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTTG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGGTTCG CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF
101 RQDAAKPRRF GGKSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASAVCPAAGPMPS
              |||||
g542      MPKWSRIRRC SVLSLMFSAAVSRLTWCAPPSNAAFVRRLKSSDGIASASAVCPAAGSMPS
              10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASXRNVS PKCPFGTAFRQDAAKPRRF GGKSHILTGSRX

```


a542.seq

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

m542/a542 94.6% identity in 111 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

957280A2 | >

```

51  AAALVGGKVH IDGLLTGDAD FGTD DDFLAA LIDDGIVFDV DGRVFEFQHR
101 AGIGADQOGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
151 ACRSRVAAFE DGQNLGCVLA DLSHCVGRGG KCHADAQNTD AQCADEGGFF
201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQN HCRTGYGDGV
251 AGSKVFRIAA LLQPDVLFQA KSRSQDLRGN VTAELILAVQ IKAHPRLIGF
301 RVKPSADAP DQYACGFDGG IDLQTADVAE IGINGVSFVR TAERRAARHA
351 ESEKGNRRRA DQDEQSDPKF QYVLH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

```

m543.seq
1  ATGTTTGTTC GGTTATTTGC CGCCGTTTTT GGCTTTCAAC TCGGCAATCA
51  GTCCGTCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 GTACGCCGAC TTCGGCGCGG ACATGATTTT CTTTGCCGCC TTTATTGACG
251 ATGGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATTCTTTG GCCAACGCTT
351 GTTTTGTGCG GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTGT
451 GCGAGCGGTG TTGGCATCGC CGTTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGCTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
601 CATGATTAAG TGTCTAGT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCCGC ATTGCCGCCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTGCGCGA TAAGGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTGC
851 CTGCTGAAT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTGCGG TCAAGTCCGA TAGCGCCGAC GCGCCGACC AATACGCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAACCG CGTAAGTTTT GTCCGAACCG CCGAACGCC CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCG CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTCT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

```

m543.pep
1  MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFPLPGYAD FGADDDFFAA FIDDGIVFDV DVGVFQFQHR
101 AGIGADQOGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 ASGVGIAVFX DAQYLSGVLT DLAYRVGRGG KCHADAQNTD AQCADEGGFF
201 HDXVSXFEYD GIRLFGGFFR IAAVGIFLGR TRHEFADKVF QNHCRGTGYD
251 GVAGSKVFRV AALLQPDVLL AQKSRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEINGVSF VRTAERRTAG
351 HAESEKGNRR RANQDEQSDP KFQYVLLH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

```

m543/g543
10      20      30      40      50      60
m543.pep MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVGGKVH
10      20      30      40      50      60

70      80      90      100     110     120
m543.pep VDGFPLPGYADFGADDDFFAIFIDDGIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR
:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g543      IDGLLTGDADFGTD DDFLAA LIDDGIVFDVDGRVFEFQHRAGIGADQOGLKFFGQRLFLR
70      80      90      100     110     120

130     140     150     160     170     180

```

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```

m543.pep  VVRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
          ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543       VVRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
          130      140      150      160      170      180

          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIA AVGIFLGKTRHEFADKV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543       KCHADAQNTDAQCADEGGFFHDV---FPENGCVCLFCGGFFRIAALSVFLGEAGHEFTDQV
          190      200      210      220      230

          240      250      260      270      280      290      299
m543.pep  FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543       FQNHCRITGYGDGVAGSKVFRIAALLQPDVLFQKRSQDLRGNVTAEILILAVQIKAHPRL
          240      250      260      270      280      290

          300      310      320      330      340      350      359
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRTAGHAESEKGNR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g543       IGFRVKPDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRAARHAESEKGNR
          300      310      320      330      340      350

          360      370      379
m543.pep  RRANQDEQSDPKFQYVLLHX
          ||||:|||||:|||||:|||||:
g543       RRADQDEQSDPKFQYVLFHX
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1   ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTGCGC GTCGGACGCG GTGCGCCAAG GGTGCGCGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTGT
451 CGGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTTGAGTGG
501 CTTTTTGACG GATTTGGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCCGCGC TCGGCATTTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG
851 CTGCTGAAC TACTTGGC GTCCAAATCG AGGCGCACCC TCGCTGATA
901 GGATTTGCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1   MAYGLLAAVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VVRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLTD LVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRITGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAEELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTDV AEIGINGVSF VRTAERRTAG

```

351 HAESEKGNRR RANQDEQSDP KFQYVLFH*

m543/a543 96.0% identity in 378 aa overlap

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
a543	MAYGLLAAVXSLQLXNQSVAHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAAFIDDGIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR					
a543	VDGFLPGXADFGADDDFFAAFIDDXIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG					
a543	VGRGAPRVADRQCGHTLEIEIGNRIGFGFLAGGVGITAFXDAQYLSGVLTDLVYRVGRGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGI RLFGGFFRIA AVGIFLGKTRHEFADKVF					
a543	KCHADAQNTDAQCADEGGFFHDXVSXFEYDGI RLFGGFFRIA AVGIFLGKTRHEFADKVF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNHCR TGYGDGVAGSKVFRVAALLQPDVLLAQKSR SQDLRG NVAELILAVQIEAHPRLI					
a543	QNHCR TGYGDGVAGSKVFRVAALLQPDVLLAQKSR SQDLRG NVAELILAVQIEAHPRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDGGIDLQ TADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
a543	GFRVKSDSADAPDQYACGFDGGIDLQ TADVAEIGINGVSFVRTAERRTAGHAESEKGNRR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQDEQSDPKFQYVLLHX					
a543	RANQDEQSDPKFQYVLFHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1585>:

g544.seq

```

1  atgaaaaaaa tactcaccgc cgccgccgctc gcactgatcg gcatacctct
51  cgccaccgctc ctcatccccg acagtaaaac cgcgcccgcc ttctccctgc
101 ccgacctgca cggaaaaacc gtttccaacg ccgacctgca aggcaaagtc
151 accctgatta atttttggtt tccctcctgt ccgggttggtg tgagcgaaat
201 gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251 tcctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301 gtcaaagact acggactgcc gtttaccgctc atttatgatg cggacaaagc
351 cgtcggacag gcattcggca cacagggtta tccgacttcc gtccttatcg
401 gcaaaaaagg cgaaatcctc aaaacttatg tcggcgaaac cgatttcggc
451 aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:

g544.pep

```

1  MKKILTA AAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
51  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIKKGEIL KTYVGEPDFG

```

m544 . seq

1	ATGAwAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCmTCCCCG	ACAGCAAAAC	CGCGCCCGCC	TTCTCCmTGC
101	CCGACCTGCA	CGGAAAAACC	GTTTCCAACG	CCGACCTGCA	AGGCAAAGTA
151	ACCCTGATTA	ATTTTTGGTT	TCCCTCCTGT	CCGGGTTGTG	TGAGCGAwAT
201	GCCCAAAATC	ATTA AAAACGG	CAAATGACTA	TAAAwCAAA	AACTTCCAAG
251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	GCGTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAATAAGG	CGAAATCTTC	AAAACCTACG	TCGGCGCAACC	CGATTTCCGGC
451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCGCAATAG	

m544 . pep

```

1  MXKILTAAVV  ALIGILLAIV  LXPDSKTAPA  FSXPDLHGKT  VSNADLQGVK
51  TLINFWFPC  PGCVSXMPKI  IKTANDYKXK  NFQVLAVAQP  IDPIESVRQY
101 VKDYGLPFTV  MYDADKAVGQ  AFGTQVYPTS  VLIGK*GEIF  KTYVGEPDFG
151 KLYQEIDTRV  AQ*

```

ORF 544 shows 90.7% identity over a 162 aa overlap with a predicted ORF (ORF 544.ng) from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544.pep	MXKILTAAVVALIGILLAIVLXPDSKTAPAFSXPDLHGKTVSNADLQGVTLINFWFPSC					
	:					
g544	MKKILTAAVALIGILLATVLIIPDSKTAPAFSLPDLHGKTVSNADLQGVTLINFWFPSC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVSXMPKIIKTANDYKXKNFQVLAVAQPIDPIESVRQYVKDYGLPFTVMYDADKAVGQ					
	: :					
g544	PGCVSEMPKVTKTANDYKKNKDFQVLAVAQPIDPIESVRQYVKDYGLPFTVIYDADKAVGQ					
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQVYPTSVLIGKXGEIFKTYVGEPDFGKLYQEIDTRVAQX					
	:					
g544	AFGTQVYPTSVLIGKKGEILKTYVGEPDFGKLYQEIDTALAQX					
	130	140	150	160		

a544.seq

1	ATGAAAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCCG	ACAGCAAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAAANC	GTTTNC AACG	CCGACCTTGA	AGGCNAAGTT
151	ANCCTGATTA	ANTTTTGGTT	TCCCTCCTGT	CCGGGTGTG	TGAGCGAAAT
201	GNCCANAATC	ATTA AAAACG	CAATGACTA	TAAAAACAAA	AACTTCCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	CGGTTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAAAAGG	CGAAATCCTC	AAA ACTTATG	TCGGCCTAAC	CGATTTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

a544.pcp

1 MKKILTAADV ALIGILLAIV LIPDSKTAPA FSLSLHGXKX VVNADLQGXV
51 XLIXFWFSPC PGCVSEMXXI IKTANDYKNK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPEFG

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTA	AVVALIG	ILLAIVL	XPDSKT	APAFSXP	DLHGKT
a544	MKKILTA	AVVALIG	ILLAIVL	IPDSKT	APAFSL	SXLHGK
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMPKII	KTANDY	KXKNFQ	VLAVAQ	PIDPIE
a544	PGCVSE	MXIIKT	ANDYKN	KNFQVL	AVAQPI	DPIESV
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQV	YPTSVL	IGKXGE	IFKTYV	GEPDFG	KLYQEI
a544	AFGTQV	YPTSVL	IGKKGE	ILKTYV	GEPDFG	KLYQEI
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgccccaaat
51  cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gccttttttta
101 cgcagatgaa acagcgggtgc gggtgggtct gctcggttgg atattctcgtt
151 gatataattta caagatgctgc cttcgagatt ccgaaccgct cctttaaaga
201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cattacttcc ccttactcag aaaatattta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaacggaa
401 aaaagcgggt tggtttttgt tggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNL PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq

```

1  ATGTTCTGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTSTA
101 CGCAGATGAA ACAGCGGTGC GGTTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCTC CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTwTTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTTGTTTTT TGTTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXCVCKV ELLTILVKNL SPNGKKRFV CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
g547	ELLTILVKNLSPNGKKRFVFCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTTCTAGT  ATAACGGATT  TAATAAAACG  GTAGCGAGTT  TTGCCCAAAT
51  CGTCGAAACT  TTCGACGTAT  TCTTCTTTAG  GAACAATTGC  ACCTTTTTTA
101 CGCAGATGAA  ACAGCGGTGC  GGTGGGTCT  GCTCGTTGGT  ATATCTCGTT
151 GATATCTTTC  CAAGATGCGG  CTTGAGATT  CCGAACCGCT  CCTTTAAAGA
201 GCTTGGGCTT  TTGATACAGA  TAAGTCTGTC  GGAACGTTT  AGGACTAATG
251 CCGAAGTCGA  GATAGATGCT  CATTACTTCC  CCTTACTCAG  AAAATATTTA
301 AAATTTATAA  TGTTACATAT  ATTTACAAAT  ATTAAAGTTT  TTTT.TGTGT
351 GTGCGTCAAG  GAATTGTTGA  CAATTTTAGT  T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT  VASFAQIVET  FDVFFFRNNC  TFFTQMKQRC  GWVCSLVYLV
51  DIFPRCGFEI  PNRSFKELGL  LIQISLSERF  RTNAEVEIDA  HYFPLLRLYL
101 KFILHIFTN  IKVFXCVCVK  ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg  taccgcggtc  ctttttgccg  ggcgttttcc  tacttgccgc
51  gcttgccgcc  tgcaaaccct  aagacaacag  tgcggcgcaa  gccgcttctt
101 caagtgcac  cgcgcgggct  gcggaataat  cggcaaaagg  gcaaaccgca
151 ggtacggata  tgcgtaagga  agacatcgcc  ggcgatttca  cactgaccga
201 cggcgaaggc  aagcctttca  gcctgagcga  tttgaaaggc  aaggctcgta
251 ttctgtcttt  cgcgttttac  cactgtcccg  atgtctgccc  gacagggtt
```

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcggcc aaaacctgcc ggtcatcaag cagcaatacc gcgtgggttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccgggtgc gtatcttatc gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCG TACCGCGTTC CTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTC ACGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTGAAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
	:					
g548	MFSVPRSFLPGVFVLAALAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKVV					
	:					
g548	GDFTLTDGEGKPFSLSDLKGKVVILSFGFTHCPDVCPTGLLTYSDTLKQLGGQAKDVKVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
	:					
g548	FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

827

	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```
a548.seq
1  ATGTTTTC CG TACCGCGTTC CTTTTTGCCG GCGGTTTTTCG TACTTGCCCG
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGCTAAGGA AGACATCGGC GCGGATTTCA CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAATATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```
a548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*
```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
a548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV					
a548	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
a548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGDQNLPIVKQQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```
g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc
```

q550.pep

1	MITDRFHLFH	FPVSFIYQSD	NKMPPENSSD	GILTTNGLQL	PFAQLGSVSF
51	QICNRTGCHA	AFHRCFGGSR	SDARQQAGIE	RSRNQVFRAE	FEFLTMSGNH
101	FFGYFFHRQI	CQSIHAGAFH	FFVDGGCADI	QRAPEDEREA	QYVVLVREV
151	GAAGTDNHVR	TGFFRQRRQD	FRIRVGHGEH	DGFFVHRVQH	FRRQQVCAGE
201	AQEDVFAFNR	IGKYAPAVVF	NGVEFFGFVH	AVFVFAGLVN	HAFGVANGYV
251	FTFQAQIQQL	VQAGNRGGTC	AGAHQSRFFD	FTAGITQGVQ	YGGGGNDGRA
301	VLVIMQYQGF	AAFA*			

m550.seq (partial)

1	..GACGGCATCG	GCAAGCACGC	GCTGGCCGTT	GTCTTCAATG	GCGTAGAACT
51	GTTTGGACTC	GTCCATACGG	TCTTTGTCTT	CGCGGGTTTG	GTAAATCACG
101	CCTTTGGAGT	CGCAAACGGT	CACGTTTTCG	CGTTTCAAGC	CCAAATCCAG
151	CAATTGGwTC	AAGCAGGCAA	TCGCGGCCGC	ACCTGCGCCG	GAACACACCA
201	AAGTCGCTTC	TTCGATTTTA	CGGCCGGTAA	AACGCAkGGC	GTTCAATACG
251	CGCGGCGCGG	TAATGATGGC	CGTCCCGTGC	TGGTCGTCGT	GGAATACGGG
301	GATTTTGCAG	CGTTTGCCTA	A		

m550.pep (partial)

```

1      ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
51     QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101    DEAAFA*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m550/g550

		10	20	30	
m550.pep		DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN			
		:: : : :			
g550	DGFFVHRVQHFRRQQVCAGEAQEDVFAFNRI GKYAPAVVFNGVEFFGFVHAVFVFAGLVN				
	190	200	210	220	230
	240				
	40	50	60	70	80
m550.pep	HAFGVANGHVFAFAQI IQQLXQAGNRGR TCAGTHQS RFFDFTAGKT XGVQYGGGNDGRA				
	:: : :				
g550	HAFGVANGYVFTFOAQI IQQLVQAGNRGGTCAGAHQS RFFDFTAGIT QGVQYGGGNDGRA				
	250	260	270	280	290
	300				
	100				
m550.pep	VLVVVEYGDFAAFAAX				
	:::				
g550	VLVIMKYGDFAAFAAX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCACA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCACGGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGGC AGGATTTCAG GATTCGGGTT GGCCATAGCG AACACGATGG
501 GTTTTTTCGT CATGGTGTTC AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTCGC GTTTCAGGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTCGTCGTG GAATACGGGG ATTTTGCAGC GTTTCGCTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGSSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQTAE DEREAQYIVH LVREVGAACT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIKHA
201 LAVVFNGLV FGLVHTVVFV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```
m550.pep
10 20 30
DGIGKHALAVVFNGVELFGLVHTVVFVAGL
|||||
a550
EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVVFVAGL
170 180 190 200 210 220

40 50 60 70 80 90
VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGGGGNDG
|||||
a550
VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGGGGNDG
230 240 250 260 270 280

100
RAVLVVVEYGDFAAFAX
|||||
a550
RAVLVVVEYGDFAAFAX
290 300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttgga cgttggtgcg
101 atacgcagaa tttcgaccgg gatataaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcggtat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccgta aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcggtca gtccgtcggt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcggtatc ttggactgca
```

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
501 acggcgcatc atctgcggcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA
201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCCGTCGTA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGKNPDAK CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	: : : : : :					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	: : : : :					
g552	ALAEMPEAKKDQAAEFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAK					
	: : : : :					
g552	YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
	190					
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
151 AATGCCGGAT TTAAACCGTA TCGGACAAA GCCCTTGCCG AAATGCCGGA

```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAAGA TTTGATTACG CCCGAAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCCGTA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

```

              10      20      30      40      50      60
m552.pep      IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
              |||
a552           IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTONFDRDIEKNMIEGFNAGFKPYADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m552.pep      ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              |||
a552           ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF
              70      80      90      100     110     120

              130     140     150     160     170     180
m552.pep      YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              |||
a552           YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG
              130     140     150     160     170     180

              190
m552.pep      CKQAGQVGKRHQKX
              |||
a552           CKQAGQVGKRHQKX
              190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CCGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFYGSPVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

```

1 TTGAATATTA AACTGAAAAC CTTGTTATG CCCTTCGCCA CGCTGGCATT
51 GTGCACCAAT GCTTTTGCCG CCCCGCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1 LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLKNAREI YTQEEIDGMI AFGSPVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAKKDQAAEAFN RYRENVLKDL ITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEAFN RYRENVLKDL ITPEVKQAVRNTLLKNAREIYTQEEIDGMI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a552-1.pep	AFYGSVPVQGSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
m552-1	AFYGSVPVQGSVVAKNPRLIKKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
	130	140	150	160	170	180
	190					
a552-1.pep	AGCKQAGQVGKRHQKX					
m552-1	AGCKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1 atggattatc tgcaaacct gtctttgggc ttgacaaaa agctgcccg
51 tatactgcaa acagaagtag cggagtgtg cttggcatgt ctagcggctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatt gggctgacgg gacgggcgtt gaggctggat ttagacgaat
251 tgggcagttt ggcgcctgcc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgcaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtttcgaggc aggggaagaa
451 aagcaggaaa tccgcatact acccatgttg cgcgggattt ctgggctggg
501 gcggaacatt tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaat catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccgg ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

m553.seq (partial)

1	ATGGATTATT	TATCAAGACT	GTCCTTTGGA	TTTAACAAAA	AGCTACCTGT
51	CATTCTGCAA	ACAGAAGTTG	CTGAATGTGG	TTTAGCATGC	CTGACATCCA
101	TCTTGTCTTA	TTATGGCTTT	CACACTGATT	TAAGAACGTT	ACGCCAAAAA
151	TACACCCTGT	CATTAAGGG	CGCAAATCTT	GCAGACATCA	TGAGATTTGG
201	CAATGAAATG	AATTTAAACG	CACGAGCTTT	GCGTTTAGAG	TTAGATGAGC
251	TGTCAAATTT	ACAACCTACC	TGCATTCTCC	ATTGGAACCT	AAACCATTTT
301	GTTGTACTTT	GTTCCATTTT	CAAAGACAGT	ATCGTCATTA	TGACCCTGTC
351	TGTCGGTATG	CGAAAAATCA	AAATGGACGA	AGTTTCACAA	AAATTCACAG
401	GGATTGCCCT	AGAATTATTC	CCCAATACCC	ATTTTGAAGA	GAAAAAAGAA
451	ACAAAGAAAA	TCAAATATTT	ATCTCTATTA	AGGGGGGG. T	CAGGCTTAAA
501	ACGCTCTTTA	ATTCAAATGC	TTATATTAGC	TATTTCTTTG	GAAGTCTTTG
551	CATTG...				

m553.pep (partial)

```

1  MDYLSRLSFG FNNKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRTLRLQK
51  YTSLSLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
101 VVLCSSISKDS IVIMDPAVGM RKIKMDEVSO KFTGIALELF PNTHFEKKE
151 TTKIKILSL  LGXSGLKRS  IOMLILAI  EVFAL...

```

Homology with a predicted ORF from *N. gonorrhoeae*

m553/q553

		10	20	30	40	50	60
g553.pep		MDYLQNL	SLGLTKKLP	VILQTEVA	EACGLACLA	AVAGFYGFY	TDLRALRSKYCLSLKGENL
		:	: ::			::	: : : : : :
m553		MDYLSRL	SFGFNKKLP	VILQTEVA	EACGLCLTS	ILSYYGFT	DLRTLRLQKYTL
		10	20	30	40	50	60
		70	80	90	100	110	120
g553.pep		ADIVRFAD	DMGLTG	RALRLDL	DELGSLRL	PCILHWD	LNHFVVLESVSSDGA
		: :	: : :	: :	:	:	: : : :
m553		ADIMRFG	NEMNLTP	RALRLDL	ELSNLQL	PCILHWN	LNHFVVLCSISKDS
		70	80	90	100	110	120
		130	140	150	160	170	180
g553.pep		RKVKTEE	ISRKFTG	IALELWP	NTRFEAGE	EKKQEIRI	LPMRLRGISGLGR
		:	: : :		: : :	:	: : : : :
m553		RKIKMDE	VSQKFTG	IALELFP	NTHFEEK	KETKKIKI	LSLLRGXSGLKRS
		130	140	150	160	170	180
		190	200	210	220	230	240
g553.pep		EVFAFLQ	NVSFKIG	RGESLAL	IGRSGCG	KSTLLDIL	SGNLPPE
		:					
m553		EVFAL					

a553.seq

1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTTGGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

a553.pep
1 MPHLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
51 Y

m553/a553 62.7% identity in 51 aa overlap

```

      10          20          30          40          50          60
m553.pep MDYLSRLSFGFNKKLPVILQTEVAECGLACLTSLSYYGFTDLRTLRLRQKYTLSLKGANL
|::||:::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
a553 MPHLQNLSLGLKKKLPVILQTEISECGLACLAAGVAFHGFHTNLRALRSKY
      10          20          30          40          50
      70          80          90         100         110         120
m553.pep ADIMRFGNEMNLTPRALRLLEDELSNLQLPCILHWNLNHFVVLCISKDSIVIMDPAVGM

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

g554.seq.

```
1 atgacagcac ataaaatcct gccgcgtcctt ctccccatca tcttaggcgt
51 ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacg
101 ccgccccccac gctccaaaca ccggaaccc tccgcgcggc acacatcgtt
151 atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
201 tgtcgaaaccg cggcgactaa cccaactgat gcacgcatac ttggttttca
251 aaaacatgaa atcgggaaat atccaatctg aagaaaaactt aaaaataccc
301 gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
351 tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
401 acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
451 aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gratgaagaa
501 caccgtatct aaaaaccgca caggcttggg tagagaagga caggtttcca
551 ccgccaaga cctctccctg ctgtctgaag cattgatgcg cgactttccg
601 gaatattacc cgctgttttc catcaaactg ttcaagtttg aaaaataga
651 acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
701 tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
751 tccgggaaccg gcaggcacat ccttgtcatc acataggtt cggaatccgg
801 ggaaaccgcg gcatcggaca acagcaagct gctgaaccgg gcattcgaatc
851 ccttcgatac gcccaaaata tatccgaag gcaaaaccgt tgcccaagc
901 caaatttccg gaggcagcaa aaaaaccgtc cgcgcaggct tctc aaaga
951 agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
1001 tggaaaccat acagccgatt ccgccccgg taaaaaaagg gcagatttta
1051 ggaaaataca aaatcaggca aaacggacat accattgccg aaaaagaaat
1101 cgtcgcatct gaaaacgtag aaaaaagaag ccggtggcaa aggttttga
1151 cgcgtctgac agqcaqtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

g554.pcp. .

1	MTAHKILPVL	LPIILGVSHA	TAASPAPNRP	TVHAAPTLQT	PETLTAAHIV
51	IDLQSRQTLS	AKNTNTPVEP	AALTQLMTAY	LVFKNMKSGN	IQSEENLKIP
101	ESAWASEGSR	MFVRPGDTVS	TDKLLKGMIA	LCANDAALTL	ADRLNGNSIE
151	NFVQQMNKEA	RRLGMKNTVF	KNPTGLGREG	QVSTAKDLSL	LSEALMRDFP
201	EYYPLFSIKS	FKFENIEQNN	RNILLYRDNN	VNGLKAGHTE	SGGYNLAVSY
251	SGNGRHILVI	TLGSEAETR	ASDNKSKLLN	ALQAFDTPKI	YPKGKTVAQI
301	QISGGSKKTV	RAGFLKEAYI	TLPHKEAKMA	EQILETIQPI	PAPVKKGQIL
351	GKIKIRQNGH	TIAEKEIVAL	ENVEKRSRWQ	RLWTRLTGO*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

m554.seq..

```
1  ATGACAGCAC ATAAAATCCT GCCCGTCTCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCGCGGCC CAACAGACCG ACGGTACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAGACAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTGAAACCG CGGGCACTAA CCCAATGAT GACCGCATAT CTGGTTTTC
251 AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCT AAAAATACCC
```



```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTGTC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAAATTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTVS TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPFLSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKI KIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTQ PETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554.pep	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
g554	AKNTNTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKI PESAWASEGSRMFVRPGDTVS					
	70	80	90	100	110	120
m554.pep	TDKLLKGMIALSANDAALTLAGRLNGSIE NFVQQMKEARRLGMKNTVFKNPTGLSREG					
g554	TDKLLKGMIALCANDAALTADRLNGSIE NFVQQMKEARRLGMKNTVFKNPTGLGREG					
	130	140	150	160	170	180
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554.pep	SGGYNLAVSYSGNRRHILVITLGSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
g554	SGGYNLAVSYSGNRRHILVITLGSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300

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```
g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 . pep QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRONGY
           |||
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRONGH
           310      320      330      340      350      360

           370      380      390
m554 . pep TIAEKEIVALENVKKRSRWQRLWACL TGQX
           |||
g554      TIAEKEIVALENVKKRSRWQRLWTRLTGQX
           370      380      390
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```
a554 . seq
1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCAGCA  ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCAC  GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAACA  TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
251 AAAACATGAA ATCGGGAAT  ATCCGATCTG AAGAAACTT  AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTGTAC  GTCCCGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG  CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT  GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATC  AAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCAG  CTGTCTGAAG CATTGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTT  CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTGATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAAGTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA  TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCGGATT CCCGCCCCAG TAAAAAAGG  GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```
a554 . pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKS GN IRSEENLKIP
101 ESAWASEGSR MFVRPGD TVS TDKLLKGMIA LSANDAAL TL AGR LGNGSIE
151 NFVQQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SNGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*
```

m554/a554 99.2% identity in 389 aa overlap

```
           10      20      30      40      50      60
m554 . pep MTAHKILPVLLSIILGVSHATAASPAPNRPTVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPTAHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep AKNINTPVEPAALTQLMTAYLVFKNMKS GN IQSEENLKIPESAWASEGSRMFVRPGD TVS
           |||
a554      AKNINTPVEPAALTQLMTAYLVFKNMKS GN IRSEENLKIPESAWASEGSRMFVRPGD TVS
```

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	TDKLLKGMIALSANDAALTLAGRLGNGSIENFVQQMNKEARRLG MKNTVFKNPTGLSREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASNKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPI PAPVKKGQILGKIKIRQNGY					
	310	320	330	340	350	360
m554.pep	370	380	390			
a554	TIAEKEIVALENVKKRSRWQRLWACLTGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatacctgct tgcgcgcgtc atcgtcgccc cgcgtgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgaaacgtc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgcgcta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcgggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQORQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC GCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAaaaaaatt
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCGATCTGCT
301 CTGTGCAAAA AATGTTCGGT GGACGAGGCG CACGCTATGT TCAaaaaaacg
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQORQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
g556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
g556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAAAC	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTTTA	AGCCTCATT	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT
201	CGACATCGAT	CCCGAAAAAG	GCAGAAATCAA	CGAGGCAAAC	CTGCGCCGTA
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC
301	CTGTCGCAAA	AATGTTCCGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC
401	AGAAACGTCC	GCACCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKTCLRGLG	GLILLTTAVL	SLIIVLIVDS	WPLAILLAAV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HOKDAITLIC
101	LSQKCSVDEA	HAMFKKRPTR	QEINQMAAKQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
a556	MDNKTCLRGLGILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAKQSRGQKRPHRX					
a556	QEINQMAAKQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

g557.seq

```

1  atgaacaaaa tattccttac tgccgcagcc ttggtgctgg gcgcgtgcgg
51  tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
101 gctggcacat cgaaggcgga caggcattgc aatttccttt ggaaaccgcg
151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accgttaccc
251 gtgcggcagt catcaacgaa tatcttttga tattgacggt tgaagcgcag
301 gtattgaaac gcggcgagcc ggtcggcaaa ccatgaccg tgtccgtccg
351 ccgcattttg gattatgccg acaacgaaat tttgggcaaa caggaagaag
401 aagaaaccct gtggcgga atgcggcagg atgttgccga acagattgtc
451 cgccgcctga cctttctgaa ggcggaatga

```

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

```

1  MNKIFLTAAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEVPGK PMTVSVRRIL DYADNEILGK QEEEETLWAE MRQDVAEQIV
151 RRLTFLKAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

```

1  ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
51  TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTTT GGAAACCGCG
151 CTGTATCAGG CTTCGGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCCGTAAA CCGATGACCG TGTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTTCTGAA GGCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..

```

1  MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
51  LYQASGRVDD AAGAQMTRLI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEVPGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAEQIV
151 RRLTFLKAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA LYQASGRVDD					
	: :					
g557	MNKIFLTAAA LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLIDSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGEVPGK PMTVSVRRVL					
g557	AAGAQMTRLIDSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGEVPGK PMTVSVRRIL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGK QEEEAALWAE MRQDAEQIV RRLTFLKAE X					
	:					
g557	DYADNEILGK QEEEETLWAE MRQDVAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

```

a557.seq
  1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCCAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCCGCAAA CCGATGACCG TGTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTTCTGAA GCGCGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

```

a557.pep
  1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQM TLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEPV GK PMTVSVRRVL AYADNEILGK QEEEEALWAE MRQDAAEQIV
151 RRLTFLKAE*

```

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA LYQASGRVDD					
a557	MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA LYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQM TLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGEPV GK PMTVSVRRVL					
a557	AAGAQM TLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ VLKRGEPV GK PMTVSVRRVL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGK QEEEEALWAE MRQDAAEQIV RRLTFLKAE X					
a557	AYADNEILGK QEEEEALWAE MRQDAAEQIV RRLTFLKAE X					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

```

g558.seq..
  1 ATGGATGCTT GTTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

```

g558.pep..
  1 MDACFFVIPA QAGIRREGIV FKRSGRILAG AGMMPLYTFS ELYMLQQGTA
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP
101 LSDGIV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

```

m558.seq..
  1 ATGAATGCTT GTTTTTTCGT CATTCCACAC CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
301 CTTTCAGACG GCATTGTTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

m558.pep..

1 MNACFFVIPT QAGIRRFIV FKRSGRILAG AGMMPYTFSELYMFQOQGT
 51 HQAPHCVLPE RDYPPIRFYR HKQTGFNRKG MGIKSISDIX RAMPSENQSP
 101 LSDGIV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPYTFSELYMFQOQGT	HQAPHCVLPE				
g558	MDACFFVIPAQAGIRRFIVFKRSGRILAGAGMMPYTFSELYMLQOQGT	HQAPHCVLPE				
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGFNRKGMGIKSISDIXRAMPSENQSPLSDGIVX					
g558	RGCPPIRFYRYKQTGFNRKGMGIKSISDTSRAMPSENQSPLSDGIVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

a558.seq

1	ATGAATGCTT	GTTTTTTCGT	CATTCCCACA	CAGGCGGGAA	TTCGGAGATT
51	CGGGATTGTT	TTCAAACGTT	CGGGTCGGAT	TCTTGCCGGT	GCGGGAATGA
101	TGCCCTTATA	TATAGTGGAT	TAAATTTAAA	TCAGGACAAG	GCGACGAAGC
151	CGCAGACAGT	ACAAATAGTA	CGGCAAGGCG	AGGCAACGCC	GTACTGGTTT
201	AAATTTAATC	CACTATACTT	TCTCCGAGCT	TTATATGTTT	CAACAGAGGA
251	CGGCACATCA	AGCACC GCAC	TGCGTGTTGC	CCGAACGAGA	CTGCCCTCCG
301	ATTAGATTCT	ATCGCTATAA	ACAGACGGGT	TTCAACCGAA	AAGGAATGGG
351	AATGAAGTCC	GTTTCCGACA	CCTCTCGGGC	GATGCCGTCT	GAAAACCAAT
401	CTCCACTTTC	AGACGGCATT	GTTTAG		

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pep

1	MNACFFVIPT	QAGIRRFIV	FKRSGRILAG	AGMMPYIVD	*I*IRTRRRS
51	RRQYK*YGKA	RQRRTGLNLI	HYTFSELYMF	QORTAHQAPH	CVLPERDCPP
101	IRFYRYKQTG	FNKGMGMKS	VSDTSRAMPS	ENQSPLSDGI	V*

m558/a558 70.2% identity in 141 aa overlap

	10	20	30			
m558.pep	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPY-----					
a558	MNACFFVIPTQAGIRRFIVFKRSGRILAGAGMMPYIVDXIXIRTRRRSR	RRQYKXYGKA				
	10	20	30	40	50	60
	40	50	60	70	80	
m558.pep	-----TFSELYMFQOQGT	HQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS				
a558	RQRRTGLNLIHYTFSELYMFQOQRTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS					
	70	80	90	100	110	120
	90	100				
m558.pep	ISDIXRAMPSENQSPLSDGIVX					
a558	VSDTSRAMPSSENQSPLSDGIVX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1649>:

g560.seq

1	atgctcatca	tccgcaacct	gatttactgg	ctgatactct	gttccagcct
---	------------	------------	------------	------------	------------

```

51  gattttcctc tttcccttta tgctgctcgc ctgcctttc cgggacgggg
101 cgcacaagat ggcgcggtgc tgggtcggca tcctcaactg gtcgctcaaa
151 cacatcgctc ggctcaaata ccgcatcatc ggcgcggaac acattccgga
201 cggccccctc gtcactctgcg ccaaaccacca aagcggtctg gaaacgctcg
251 cgctccaaga gatttttccg ccgcaggttt acgttgccaa gcgcgagttg
301 ttcaaaatcc cttttttcgg ctggggcttg aaactggtca aaaccatagg
351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401 gtttggcgcg caaaaacgaa ggattattgga ttaccatttt ccccgaggc
451 acgcgccttg cgcccggaaa acgcggcaaa taaaaactcg gcggcgcgcg
501 catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601 gtcacatctc gtccgaccat cccgcacgca agcggcagcg aagccgaatt
651 gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

m560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAQHSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGCGCGGGTC TGGGTCGGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCCG CTGGGGCTTG AAACGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTGGTGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCGAAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCCTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCCG
701 GCGCAGGCCG GTTGCCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKRGK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

          10      20      30      40      50      60
m560.pep  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560      MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK HIVGLKYRII
          10      20      30      40      50      60

          70      80      90     100     110     120
m560.pep  GAENIPDRPA VICAQHSGW ETLALQDIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560      GAEHIPDRPS VICAQHSGW ETLALQEIFP PQVYVAKREL FKIPFFGWGL KLVKTIGIDR

```


843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQOPLISGAGPFAA					
g560	LNSGEFWPKNSFLKYPGEITVIICPTIPHASGSEAELEMEKCEHLIETQOPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1   ATGCTCATCA TCCGCAACCT GATTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTCCCTTTA TGCTGCTCGC CTCGCCCTTC CGAGACGGGG
101 CGCACAAAGAT GCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC CCTTTTTCG CTGGGGCTTG AAAGTGGTCA AAACCATAGG
351 CATAGACCGC AACAAACGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTTGGCGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCGCGAGCG
451 ACACGCCTTG CCGCGGAAA ACGCGGCAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCCG CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAAA TGCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCGG
701 GCGCAGGCCG GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1   MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHOSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGARMAM MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQOP LISGAGPFAA KMPSETA*

```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHOSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHOSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

844

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560						
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560						
	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```

m561.seq.
1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAG ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGC GC AATTTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCGCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGAAAATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCGTC TGTACTGATG CTGTTTGGC
551 ACCAGATTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTCCTA TCAATGGGC GGCAGGTTGA
701 AAATTTATA TGATGATTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGACGGC
901 GGATCCGATG TTTATGTTTC CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGAAGTACC ATGAGGAAAT CTTCCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGCGCAAAAC AGGAGGAAGA AAAACGCCTG CTGACAGTAT
1151 TGCAAGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAG CCGCCTTTGC
1251 CGAAAAACAA CGGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCGGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTCTT GCCGCTCAG GAAGCGCAGC TCCAAATGAT TTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTCACCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTCGACACG GAGAAAATAG GAGAACCAC GGCAGCCAT
1651 GTCGGAATGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```

m561.pep
1  MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYTQTRDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFAENK REEAENISF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLPPO EAQLQMIFIL

```

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRL	ENAASVIEEAGNLRMQAY				
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALSVVLTLLLSF	RL	ENAASVIEEAGNLRMQAY			
	10	20	30	40	50	60
m561.pep	70	80	90	100	110	120
	RLAYMAGEGSPRAQIDNQVAEF	EKSLKRIAQSDAIHPLIPSDT	PLAYDLIQSMLIIDWQA			
g561	RLAYMAGEGSPRAQIDNQIAE	EKSLKRISQSDAIHPLIPSDN	PLAYDLIQSMLIIDWQA			
	70	80	90	100	110	120
m561.pep	130	140	150	160	170	180
	HILPPLQSYRRPTQVDLYRF	AGNIELFLQALENANEKNTWWL	RRFQWAIMLMTLVSSVLM			
g561	NILPPLQAYRRPTQIELYRF	AGNIELFLQALENAGEKNTWWL	RRFQWVIMLMTLVSSVLM			
	130	140	150	160	170	180
m561.pep	190	200	210	220	230	240
	LFWHQIWVIRPLQALREGA	ERIGRRCFDIPVPEGGTP	EFKQVGRCFNQMGGR	LKILYDDL		
g561	LFWHQIWVIRPLQALREGA	ERIGQRHFDIPVPEDVR	PNSNRSGGVSTKWRSGX			
	190	200	210	220	230	
m561.pep	250	260	270	280	290	300
	EGQVAEQTRSLEKQNQNLT	LLYQTRDLHOSYIPQAA	AHFLNRLIPAVGADSG	RVCLD		

```

a561.seq
1 ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51 GAAACTCCTG ACCGGA CTGT GGGTCGGGTT GGCGGCATTG TCTGTCTGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA AC CGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA CCTTGAGAA T CGACGGCATA C CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG ACCCGTGC GC AAATTGCACA T CAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCTT
301 TCGGACACCC CTCTTGCTTA TGATTTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT CCGGAAAACA TCGAACTGTT TTTGCAAGT
451 TTGGAATAATG CCAACGAAAA AACACATGG TGGCTCAGG GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCGTC TGTA CTGATG CTGTTTTGGC
551 ACCAGATTTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTC AA TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TAGATTTTG GAAGGACAAG TCGCCGAGCA GACACGCGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAA TTACAGGGGA
801 TCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTGG GGAAGTACC ATGAGGAAAT CTTCCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTCTCTTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GGC GCAAAAC AGGAGGAAGA AAAACGCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
1251 CGAAAAACAA CCGGAGGAAG CCGCAGAAAA CATCGGCTTC ATCAAAAACAG
1301 GCGTGACAGGA ATGTTATGAA GATGTCGCGG AACTGTGCTG CAACTTCCGT
1351 ACCAAAATCA GTAATAAAGA ATTTCCCGAA CCGGTTGCCG ACCTATTCT

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFESLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMILIOWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQONQNTL LYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQGFDT ENIGEPGSGH
551 VGLHIMQERA KRIHAVLEIR SQAQQTTSV LTVASEESLK *

m561/a561 96.9% identity in 590 aa overlap

10 20 30 40 50 60
m561.pep MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY
|||||
a561 MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY
10 20 30 40 50 60

70 80 90 100 110 120
m561.pep RLAYMAGEGSPRAQIDNQVA EFESLKRIA QSDAIHPLIP SDTPLAYDLI QSMILIOWQA
|||||
a561 RLAYMAGEGSPRAQIDNQVA EFESLKRIA QSDAIHPLIP SDTPLAYDLI QSMILIOWQA
70 80 90 100 110 120

130 140 150 160 170 180
m561.pep HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
|||||
a561 HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
130 140 150 160 170 180

190 200 210 220 230 240
m561.pep LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLKILYDDL
|||||
a561 LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLKILYDDL
190 200 210 220 230 240

250 260 270 280 290 300
m561.pep EGQVAEQTRSLEKQONQNTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
|||||
a561 EGQVAEQTRSLEKQONQNTLLYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG
250 260 270 280 290 300

310 320 330 340 350 360
m561.pep GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
|||||
a561 GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT
310 320 330 340 350 360

370 380 390 400 410 420
m561.pep LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
|||||
a561 LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

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847

	370	380	390	400	410	420
m561.pep	430	440	450	460	470	480
a561	REEEAENISFIKTGVQECYEDVRELLLNFR	TKISNKEFPEAVADLFARFTQOTGITVETA				
	430	440	450	460	470	480
m561.pep	490	500	510	520	530	540
a561	WENGSLFLPPQEAQLQMIFILQESLSNIRKHARATHVKFTLSEHGGRFTMTIQDNGQGFD					
	490	500	510	520	530	540
m561.pep	550	560	570	580	590	
a561	EKIGIPTGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKK					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

```

1   atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcgccg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaaacgac ggtcatgtcg gcggtcagga cgctgtcgtt cagccgctac
301 acgacgggtg catcgacatc gtcgccgcc cggcgcgaaa tgaggacttt
351 tttcgcgccg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgcgggtcga gaagaagggg attttgcgc cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

```

1   MASPSSLPFN SGTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRTLSFTPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLPAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

```

1   ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
101 GGGCGCGCGC CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTGATGTCG GCGGTCAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TCGGGGTCGA GAAGAAGGGG ATTTTGTGCG CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACCG
551 TGTCGAATTT GGTGAGATGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

```

1   MASPSSLPFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRTLSFTPY

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848

101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS
 151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLPLAL
 201 TATSWSWS*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
g562	MASPSSLPFNSGKTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRPLALTATSWSWSX					
g562	PCTVSNLVRWALVSRPLALTATIWSWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq

1	ATGGCAAGCC	CGTCGAGTTT	GTCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCAGTTT	TGGTCGGAAT	CATGTTTTCC	ACGCCGCTGC
101	GGGCGCGGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCGAGAGGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAAACGAC	GGTCATGTCG	GCGGTCAGGA	TGCTGTGCGT	CACGCCGTAC
301	ACGACGGTTG	CATCGACATC	GTCGCCGCC	GGTGCGGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTTCCAGAT	GAACCTTGGC	TTTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCNA	GAAGAANGGG	ATTTTGTCGC	CGTTGACGAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTGCACGG
551	TGTCGAATTT	GGTGAGGTGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	TTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep

1	MASPSSLSFN	SGSTKPTAFA	APVLVGIMFS	TPLRARRRSL	WRTSVTVWSL
51	VSAWMVVIAP	LTMPTLSLNT	LATGERQLVV	QEALETTVMS	AVRMLSFTPY
101	TTVASTSSPP	GAEMRTFFAP	LSR*TLAFSL	LVNAPVHSMT	KSTPSSFHGS
151	SAGLRVXKXG	ILSPLTMLRP	PSWDTASAKR	PCTVSNLVRW	ALVSRPLPLAL
201	TATIWSWS*				

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
a562	MASPSSLSFN SGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAMVVIAP					
	10	20	30	40	50	60

849

	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSTFTPYTTVASTSSPPGAEMRTFFAP					
a562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRMLSTFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMKSTPSSFHGGSSAGLRVEKKGILSPLTMRLLPPSWDTSASKR					
a562	LSRXTLAFSLLVNAPVHSMKSTPSSFHGGSSAGLRVXKXGILSPLTMRLLPPSWDTSASKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRPLALTATSWWSX					
a562	PCTVSNLVRWALVSRPLALTATIWSWSX					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGCCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCACTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTTGGA TTCAAGCAA TCCTTGGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTGTAAC CAAATCAACA GCAGCCATCC
501 TTCACAACCT AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTTAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
701 GTTTGGATGC CCGTGATACC GATTTACACG GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTG GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCGAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTGAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACTTGC AAGCAGGAAA ACGCATTTCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTGCGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAAAC ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCACAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACCTG CGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101 GCGCGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA
2151 AACCTTTGGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAACCT
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA
2251 AATTATACTT TGCCGGAGGA AATCACACGC GACATTTTAC TGGGTTTATT
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAG CCGTCATGCG CCCAGCCAAG
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TGCGAAAAGC
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG TGACTATATG
2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT
2801 GGTGTTGACA AAAAGAAGTT AAACCTTCCTG ATGGCGGCAC ACAAACCGTA
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA
2901 AGGTGCATTG TTGTCAAGCA GCAATACACA AATCAATGTT TCAGGCAGCC
2951 TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAA AATCAGCGGT
3051 TACGGCCACA CAAGACATCA ATAATATTGG CCGCATTTCT TCTGCCGAAC
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC
3201 AGGTATTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG
3251 GCAAAGCAT CAACATCATT GCCGGTCAAA TCAGCAATCA ATCAGATCAA
3301 GGGCAAACCC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA
3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC
3401 GAGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT
3451 ACCCTatTGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG
3501 CGCAAAGGC ACACTTGCCG TGTATGCTAA AAATGACATT ACTATCAGCT
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA
3601 AGCGGCGGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA
3651 CGAAACTGCT CAAAGCAGCA CTTTGAAGG CAAGCAAGTT GTATTGCAGG
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTT CGATAATGGC
3751 ACCCGGATTC AAGCAGGCAA TCATGTTTCG ATTGGTACAA CCCAAACTCA
3801 AAGCCAAAGC GAAACCTATC ATCAAACCCA AAAATCAGGA TTGATGAGTG
3851 CAGGTATCGG CTTCACTATT GGCAGCAAGA CAAACACACA AGAAAACTAA
3901 TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCC TGAAAGGCGA
3951 TACCACCATT GTTGCAAGCA AACACTACGA ACAAACCGGC AGCAACGTTT
4001 CCAGCCCTGA GGGCAACAAC CTTATCAGCA CGCAAAGTAT GGATATTGGC
4051 GCAGCACAAA ACCAATTAAA CAGCAAAACC ACCCAAACCT ACGAACAAAA
4101 AGGCTTAACG GTGGGCATTG AGTTCGCCCG TTACCGATTT GGCACAACAA
4151 GCGATTGCCG TAGCACACA AGCAGCAAAC AAGTCGGACA AAGCAAAAAC
4201 GACCGCGTTA ATGCCATGGC GGCTGCCAAT GCAGGTTGGC AGGCCTATCA
4251 AACAGGCAAA GGCGCACAAA ACTTAGCCAA TGGTACAACC AATGCCAAAC
4301 AAGTCAGCAT CTCCATAACC TACGGCGAAC AGCAAAACCG ACAAACCACC
4351 CAAGTTCAAG CCAATCAAGC CCAAGCGAGT CAAATTCAAG CAGGCGGCAA
4401 AACTACCCTT TATTGCCGAA GGTGCGGCGA ACAATCCAAT ATCAACATCA
4451 CAGGCTCAGG TGTTTCAGGC AGAGCAGGAA CCGGCCTGAT TGCCGATAAG
4501 CAAATCCATC TGCAATCAGC CGAGCAAAGC AATACCGAAC GCAGCCAAAA
4551 CAAATCAGCA GGCTGGAACG CAGGTGCTGC CGTATCATTG GGACAAGGAG
4601 GCTGGTCATT AGGCGTTGCC GCAGGCGGCA ATGTGCGCAA AGGCTACGGC
4651 TATGGCGATA GCGTAACCCA CCGCCATAGC CATATTGGCG ACAAAGGCAG
4701 CCAAACCTT ATCCAAAGTG GTGGCGATAC CATCATCAA GGCAGCGAAG
4751 TACGCGGCAA AGGCGTACAA GTCAATGCCA AAAACCTAAG CATTCAAAGT
4801 GTACAAGATA GAGAACTTA TCAAAGCAA CAACAAAACG CCGGTGCACA
4851 AGTTACCGTA GGTATGGCT TCAGTGCCAG TGGCGATTAC AGCCAAAGCA
4901 AAATCCGAGC CGACCATGCT TCGGTAACCG AGCAAAGCGG TATTTATGCC
4951 GGAGAAGACG GCTATCAAAT CAAGGTCGGA AACCATACAG GCCTCAAAGG
5001 CGGCATCATC ACCAGCAGCC AAAGCGCAA AGACAAGGGT AAAAACCGAT
5051 TCAGCACAGG CACACTCGCC GGCAGTGATA TTCAAATTA CAGCCAATAC
5101 GAAGGAAAAA GTTTTGGATT GGGTGCCAGC GTTGCCGTAA GCGGCAAAAC
5151 ACTGGGACAG GGCGCAAAAA ATAAACCTCA AGACAAACAC CTGACAAGCA


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5201 TAGCCGATAA AAACGGCGCA AGTTCATCAG TAGGGTACGG CAGCGACAGC
5251 GACAGTCAAA GCAGCATCAC AAAAAGCGGC ATCAATACCC CCAAAAACAT
5301 TCAAATCACA GACGAAGCCG CACAAATCAG GCTGACAGGC AAAATAGCGG
5351 CACAAACCAA AGCCGATATT GATACAAACG TAACCACAGA CACCGCCGAA
5401 CGACATTTCGG GCAGCCTGAA AAACATATTT GACAAAGATA GAGTGCAAAG
5451 TGAAGTGGAT TTACAAAGaA CCGTCAGCCA AGATTTTtagT AAAAATGTTC
5501 AACAAACCAA TACCGAGATT AACCAACATT TAGACAAACT CAAAGCAGAC
5551 AAAGAAGCAG CCGAAACAGC AGCAGCCGAG GCATTAGCCA ATGGCGATAT
5601 GGAAACTGCC AAACGCAAAG CCCATGAAGC TCAAGATGCG GCAGCAAAAG
5651 CAGATAATTG GCAACAAGGC AAAGTCATT TCAACATGTT AGCCTCAGGT
5701 TTAGCTGAGC CGACCCAAAG CGGAGCgggc ATCGCTGCGG CTACCGCATC
5751 GCCagaCGTA TCGTATGCGA TTGGACAGCA CTTTAAaagT TTAGCCGGTC
5801 AAAACGCGAA TGGCAAAC TAACGCCAGTC AagaAACCGC TCACGTTCTT
5851 GCCACGCGG TATTAGGAGC AGCGGTGCGC GCAGCATGAG GCAACAATGC
5901 CCCGGCAGGA GCATTGGGTG CGGGCGGGTc ggAagcggCC GCCCAATCA
5951 TCGGCAAATG GCTGTACGGC AAAGGAGAcg gcggcagccT GAATgcggag
6001 gaaaAAGaga CCGTTTCGGC GATTACAAGG ATGCTGggtA cGgctGCCG
6051 AGCAGCTGAG GGAAACTCGT CCGCCGATGC TGTGTGGGT TGTTTTcaaa
6101 cggetTCaga TTTCGCTTCC TCTTTTTCAT ATCTATAAA CATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1666; ORF 563.ng>:

g563.pep..

```

1 MNKTLRVIF NRKRGA VAV AETTKREGKS CADSGSGSVY VKSVSFIPTH
51 SKAFCF SALG FSLCLALGTV NIAFADGIIT DKAAPKTQQA TILQTGNGIP
101 QVNIQTPTSA GVSVNQYAQF DVGNRGAILN NSRSNTQTQL GGWIQGNPWL
151 TRGEARVVVN QINSSHPSQL NGYIEVGRR AEVVIANPAG IAVNGGGFIN
201 ASRATLTTGQ PQYQAGDFSG FKIROGNAVI AGHGLDARDT DFTRILLYAN
251 KITLISTAEQ AGIRNQQLF ASSGNVAIDA NGRLVNSGTM AAANVQDMNN
301 TAEHKVNIRS QAFENSGTAV SQQGTQIHSQ SIQNTGKLLS AGTEDLAVSG
351 SLNNQNGEIA TNQQLI IHDG QQSTVVIDNT NGTIQSGRDV AIQAKSLNN
401 GTLAADNKLD IALQDDFYVE RKIVAGNELS LSTRGSLKNS HTLQAGKRIR
451 IKANNLDNAV QGNIQSGGTT DIGTQHNL TN RGLIDGQQT I QAGQMNINIG
501 TGRYKGDNIA IAATRLDNQD ENGTGAAIAA RENLNLGIEQ LNNRENSLIY
551 SGNDMAVGG A LDTNDQATGK AQRIHNAGAI IEAAGKMRLG VEKLHNTNEH
601 LKTQLVETGR ERIVDYEA FG RHELLREGTQ HELGWVFN YN ESDHLRTPDG
651 VAHENWHKYD YEKVTQETQV TGTAPAKIIA GSDLIIDSKA VFNSDSRIIA
701 GGQLLVQTEK DGLHNEQTFG EKKVFSENGK LHN YWRARRK GHDETGHREQ
751 NYTLPEEITR DISLGSFAYE SHSKALSRHA PSQGT ELPQS NRDNIRTAKS
801 NGISLPYTPN SFTPLPGSSL YIINPANKGY LVETDPRFAN YROWLGS DYM
851 LGSCLKDPNN LHKRLGDGY EORLINEQIA ELTGHRRLDG YQNDEEQFKA
901 LMDNGATAAR SMNLSVGIAL SAEQAAQLTS DIVVLVQKEV KLPDGGTQTV
951 LMPQVYVRVK NGGIDGKGAL LSGSNTQINV SGSLKNSGTI AGRNALIINT
1001 DTLDNIGGRI HAQKSAVTAT QDINNIGGIL SAEQTL LNA GNNINNQSTA
1051 KSSQNAQGS TYLDRMAGIY ITGKEKGVLA AQAGKDINII AGQISNQSDQ
1101 GQTRLQAGRD INLDTVQTK YQEIHFADN HTIRGSTNEV GSSIQT KGDV
1151 TLLSGNNLNA KAAEVGSAKG TLAVYAKNDI TISSGIHAGQ VDDASKHTGR
1201 SGGGNKLVIT DKAQSHHETA QSSTFEGKQV VLQAGNDANI LGSNVIDNG
1251 TRIQAGNHVR IGTQTQSQS ETYHQTQKSG LMSAGIGFTI GSKTNTQENQ
1301 SQSNEHTGST VGS LKGD TTI VASKHYEQTG SNVSSPEGNN LISTQSM DIG
1351 AAQNQLNSKT TQTYEQKGLT VGIQFARYRF GTTSDCRSTQ SSKQVQSKN
1401 DRVNAMAAAN AGWQAYQTGK GAQNLANGTT NAKQVSI SIT YGEQQNRQT
1451 QVQANQAQAS QIQAGGKTTL YCRRCGEQSN INITGSGVSG RAGTGLIADK
1501 QIHLQSAEQS NTERSONKSA GWNAGAAVSF GQGGWSLGVA AGGNVKGKYG
1551 YGDSVTHRHS HIGDKGSQTL IQSGGDTIIK GAQVRGKVQ VNAKNLSIQS
1601 VQDRETYQSK QONAGAQVTV GYGFSASGDY SQSKIRADHA SVTEQSGIYA
1651 GEDGYQIKVG NHTGLKGGII TSSQSAKDKG KNRFSTGTLA GSDIQNYSQY
1701 EGKSFGLGAS VAVSGKTLGQ GAKNKPQDKH L TSIADKNGA SSSVGYGSDS
1751 DSQSSITKSG INTPKNIQIT DEAAQIRLTG KIAAQTKADI DTNVT TDAE
1801 RHSGSLKNIF DKDRVQSELD LQRTVSQDFS KNVQQTNT EI NQHLDKL KAD
1851 KEAAETA AAE ALANGDMETA KRKAHEAQDA AAKADNWQQG KVI LNM LASG
1901 LAEPTQSGAG IAAATASPDV SYAIGQHF KD LAGQNANGKL TASQETAHVL
1951 AHAVLGAAVA AAXGNAPAG ALGAGGSEAA APIIGKWL YG KDGGS LNAE
2001 EKETVSAITR MLGTAAGAAE GNSSADAVWG CFQTASDFAS SFSYPINM*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

```
1   ATGAATAAAA CTCTCTATCG TGTAATTTTC AACCGCAAAC GTGGGGCTGT
51  GGTAGCCGTT GCTGAAACTA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGATTCAGG CAGCGCTCAT GTGAAATCTG TTCCTTTTGG TACTACTCAT
151 GCACCTGTTT GTCGTTCAAA TATCTTTTCT TTTTCTTTAT TGGGCTTTTC
201 TTTATGTTTG GCTGTAGGTA CGGCCAATAT TGCTTTTGCT GATGGCATTG
251 TTGCTGATAA AGCTGCTCCT AAAACTCAAC AAGCCACGAT TCTGCAAACA
301 GGTAACGGCA TACCGCAAGT CAATATTCAA ACCCTACTT CGGCAGGGGT
351 TTCTGTTAAT CAATACGCCC AGTTTGATGT GGGTAATCGC GGGGCGATTT
401 TAAACAACAG CCGCAGCAAC ACCCAAACAC AGCTAGGCGG TTGGATTCAA
451 GGTAATCCTT GGTGGCAAG GGGCGAAGCA CGTGTGGTTG TAAACCAAAT
501 CAACAGCAGC CATTCTTCAC AAATGAATGG CTATATTGAA GTGGGCGGAC
551 GACGTGCAGA AGTCGTTATT GCCAATCCGG CAGGGATTGC AGTCAATGGT
601 GGTGGTTTTA TCAATGCTTC CCGTGCCACT TTGACGACAG GCCAACCGCA
651 ATATCAAGCA GGAGACCTTA GCGGCTTTAA GATAAGGCAA GGCAATGTTG
701 TAATCGCCGG ACACGGTTTG GATGCCCGTG ATACCGATTT CACACGTATT
751 CTCAGTTATC ATTCCAAAAT TGATGCACCC GTATGGGGAC AAGATGTTCC
801 TGTGCTCGCG GGACAAAACG ATGTGGTTCG AACAGGTAAT GCACATTTCG
851 CTATTCTCAA TAATGCTGCT GCCAATACGT CAAACAATAC AGCCAACAAC
901 GGCACACATA TCCCTTTATT TGCGATTGAT ACAGGCAAAT TAGGAGGTAT
951 GTATGCCAAC AAAATCACCT TGATCAGTAC GGCCGAGCAA GCAGGCATTC
1001 GTAATCAAGG GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA
1051 AATGGCCGTT TAGTCAATAG TGGCAGCATG GCTGCCGCCA ATGCGAAAGA
1101 TACGGATAAT ACAGCGGAAC ACAAAGTCAA TATCCGAGT CAGGGCGTTG
1151 AAAACAGCGG TACGCGGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAG
1201 TCGATTCAAA ACACTGGCAC ATTATTGTCC TCAGGCGAAA TATTGATTCA
1251 CAATTCGGGC AGCCTGAAAA ATGAAACATC AGGCACCATT GAAGCCGCTC
1301 GTTTGGCTAT TGATACCGAC ACACTTAATA ATCAAGGCAA ACTCTCTCAA
1351 ACAGGTTTCA AAAAACTCCA TATTGATGCA CAAGGCAAAA TGGATAACCG
1401 TGGCCGCATG GGTTTACAAG ATACCGCACC AACCGCGTCA AATGGTTCAA
1451 GCAATCAAAAC CGCAATAGT TACAATGCAT CTTTCCATT ATCCACTACC
1501 ACACCAACAA CGGCAACAGG TACGGGTACT GCAACCGTTT CTATATCAA
1551 CATAACTGCG CCTACCTTTG CTGATGGGAC AATTTCGACT CATGGTGCAC
1601 TGGATAATTC AGGCAGTATT ATTGCCAATG GTCAAACAGA TGTTAGTGCG
1651 CAACAAGGTT TAAATAATGC AGGACAAATA GACATTTCATC AGTTAAATGC
1701 AAAAGGTTTC GCGTTTGACA ATCACAATGG AACAATTATC AGTGATGCGG
1751 TCCACATTCA AGCCGGCAGC CTGAATAATC AAAATGGCAA CATCACAACA
1801 CGCCAACAGT TAGAGATTGA AACCAGTCAA CTGGATAACG CTCATGGCAA
1851 GTTATTATCA GCAGAAATAG CGGATTTAGC CGTTTCAGGC AGCCTGAACA
1901 ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT TCACGATGGT
1951 CAGCAATCTA CCGCTGTCAT TGATAATACG AATGGCACGA TACAATCAGG
2001 CCGTGATGTT GCTATTCAGG CAAAATCGTT ATCCAACAAC GGCACACTTG
2051 CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATT TTATGTAGAA
2101 CGCAATATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC GAGGCAGCCT
2151 GAAAAATTCA CATACTTTGC AAGCAGGAAA ACGCATTTCG ATTAAAGCAA
2201 ATAACCTTGA TAATGCAGCA CAAGGCAACA TTCAATCCGG CGGTACGACA
2251 GACATTGGCA CGCAGCACAA TTTAACCAAT AGAGGCTTGA TTGACGGACA
2301 ACAAACCAA ATCCAAGCCG GGCAATGAA TAATATCGGT ACAGGTCGGA
2351 TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA CAATCAAGAT
2401 GAAAACGGTA CAGGTGCCG CATTGCCGCA CGTGAAAACC TGAATTTAGG
2451 CATCGGACAA TTAACAACCC GTGAAAACAG TCTGATTTAC AGCGGTAACG
2501 ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGGCCAAGC CACAGGCAAA
2551 GCCCAAAGGA TACACAATGC CGGCGCAACC ATTGAAGCTG CAGGCAAAAT
2601 GCGTTTtaggt GTAGAAAAGC TGCACAATAC CAATGAGCAT TTGAAAACGC
2651 AGTTGGTAGA AACAGGGCGC GAGCATATTG TTGATTACGA AGCATTTGGA
2701 CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG GCTGGTCTGT
2751 CTATAACGAT GAATCAGACC ACTTACGCAC CCCTGATGGA GCGGCGCATG
2801 AAAATTGGCA TAAATACGAT TATGAAAAAG TCACCCAAAA AACCCAAGTT
2851 ACCCAAAC TGCCAGCCAA AATCATTTCA GGTAATGATT TAACCATTGA
2901 TGGTAAAGAA GTATTTAATA CCGATAGCCA AATCATTGCT GGTGGCAATC
2951 TCATTGTACA AACAGAAAAA GACGTTTGC ATAACGAGCA AACCTTTGGC
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3001 GAAAAGAAAG TATTCAGTGA AAATGGCAAA TTACACAGCT ATTGGCGTGA
3051 GAAACATAAA GGACGAGACT CAACGGGACA TAGCGAACAA AATTACACTT
3101 TGCCGGAGGA AATCACACGC AACATTTTAC TGGGTTTATT TGCCTATGAA
3151 TCGCATCGCA AAGCATTAAG CCATCATGCG CCCAGCCAAG GCACTGAGTT
3201 GCCGCAAGGC AACGGTATTT CGCTACCCTA TACGTCCAAT TCTTTTACCC
3251 CATTACCCAG CAGCAGCTTA TACATTATCA ATCCTGTCAA TAAAGGCTAT
3301 CTTGTTGAAA CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG
3351 TGACTATATG CTGGACAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC
3401 GTTTGGGTGA TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA
3451 GAGCTGACAG GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA
3501 ATTTAAAGCC TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC
3551 TCAGCGTTGG CATTGCATTA AGTGCCGAGC AAGTAGCGCA ACTGACCAGC
3601 GATATTGTTT GGTGTTGACA AAAAGAAGTT AAGCTTCCTG ATGGCGGCAC
3651 ACAAACCGTA TTGGTGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGACA
3701 TAGACGGTAA AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT
3751 TCAGGCAGCC TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT
3801 TATCAATACC GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA
3851 AATCAGCGGT TACGGCCACA CAAGACATCA ATAATATTGG CGGCATGCTT
3901 TCTGCCGAAC AGACATTATT GCTCAACGCA GGCAACAACA TCAACAGCCA
3951 AAGCACCACC GCCAGCAGTC AAAATACACA AGGCAGCAGC ACCTACCTAG
4001 ACCGAATGGC AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA
4051 GCGCAGGCAG GAAAAGACAT CAACATCATT GCCGGTCAAA TCAGCAATCA
4101 ATCAGAGCAA GGGCAAACCC GGCTGCAAGC AGGGCGCGAC ATTAACCTAG
4151 ATACGGTACA AACCAGCAAA CATCAAGCAA CCCATTTTGA TGCCGATAAC
4201 CATGTTATTC GCGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA
4251 AGGCGATGTT ACCCTATTGT CAGGGAATAA CCTCAATGCC AAAGCTGCCG
4301 AAGTCAGCAG CGCAAACGGT ACACTCGCTG TGTCTGCCAA AAATGACATC
4351 AACATCAGCG CAGGCATCAA CACGACCCAT GTTGATGATG CGTCCAAACA
4401 CACAGGCAGA AGCGGTGGTG GCAATAAATT AGTCATTACC GATAAAGCCC
4451 AAAGTCATCA CGAAACCGCC CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT
4501 GTATTGCAAG CAGGAAACGA TGCCAAACATC CTTGGCAGCA ATGTTATTTC
4551 CGATAATGGC ACCCAGATTTC AAGCAGGCAA TCATGTTTCG ATTGGTACAA
4601 CCCAAACTCA AAGCCAAAGC GAAACCTATC ATCAAACCCA GAAATCAGGA
4651 TTGATGAGTG CAGGTATCGG CTTCACATAT GGCAGCAAGA CAAACACACA
4701 AGAAAACCAA TCCCAAAGCA ACGAACATAC AGGCAGTACC GTAGGCAGCT
4751 TGAAAGGCGA TACCACCATT GTTGCAGGCA AACACTACGA ACAAATCGGC
4801 AGTACCGTTT CCAGCCCGGA AGGCAACAAT ACCATCTATG CCCAAAGCAT
4851 AGACATTCAA GCGGCACACA ACAAATTAAC CAGTAATACC ACCCAAACCT
4901 ATGAACAAAA AGGCCTAACG GTGGCATTCA GTTCGCCCGT TACCGATTGT
4951 GCACAACAAG CGATTGCCGT AGCACAAAGC AGCAAACAAG TCGGACAAAG
5001 CAAAAACGAC CGCGTTAATG CCATGGCGGC TGCCAATGCA GGCTGGCAAG
5051 CCTATCAAAC AGGTAAGAGT GCACAAAACCT TAGCCAATGG TACAACCAAT
5101 GCCAAACAAG TCAGCATCTC CATAACCTAC GGCGAACAGC AAAACCGACA
5151 AACCACCCAA GTTCAAGCCA ATCAAGCCCA AGCGAGTCAA ATTCAAGCAG
5201 GTGGTAAAAC CACATTAATC GCCACAGGCG CAGCAGAACA ATCCAATATC
5251 AACATCGCAG GCTCAGATGT TGCCGGCAAA GCAGGCACAA TCCTGATTGC
5301 CGATAACGAC ATCACTACTC AATCAGCCGA GCAAAGCAAT ACCGAACGCG
5351 GCCAAAACAA ATCGGCAGGC TGGAACGCAG GTGCTGCCGT ATCATTCGGA
5401 CAAGGAGGCT GGTCAATTAG CGTTACCGCA GGCGGCAATG TCGGCAAAGG
5451 CTACGGCAAT GCGACAGCA TCACCCACCG CCATAGCCAT ATCGGCAGCA
5501 AAGGCAGCCA AACCCCTTATC CAAAGCGGTG GCGACACTAC CATCAAAGGC
5551 GCGCAAGTAC GCGGCAAAGG CGTACAAGTC AATGCCAAAA ACCTAAGTAT
5601 TCAAAGCGTA CAAGATAGAG AAACCTATCA AAGCAAACAA CAAAACGCCA
5651 GTGCACAAGT TACCGTAGGT TATGGCTTCA GTGCCGGTGG CGATTACAGC
5701 CAAAGCAAAA TCCGAGCCGA CCATGTTTCA GTAACCGAGC AAAGCGGTAT
5751 TTAGTCCGGA GAAGACGGCT ATCAAATCAA GGTCGGAAC CATAAGAGC
5801 TCAAAGGCGG CATCATCACC AGTACCCAAA GCGCAGAAGA CAAGGTAAA
5851 AACCGCTTTC AGACGGCCAC CCTCACCCAT AGCGACATCA AAAACCCAG
5901 CCAATACAAA GCGGAAAGTT TTGGATTGGG CGCAAGTGCG TCCATAAGCG
5951 GCAAAACACT GGGACAGGGC GCACAAAATA AACCTCAAAA CAAACACCTG
6001 ACAAGCGTAG CCGATAAAAA CAGCGCAAGT TCATCAGTGG GTTATGGCAG
6051 CGACAGCGAC AGTCAAAGCA GCATCACAAA AAGCGGCATC AACACCCGCA

6101 ACATTCAAAT CACCGACGAA GCCGCACAAA TCCGGCTGAC AGGCAAAACA
 6151 GCGGCACAAA CCAAAGCCGA TATTGATACA AACGTAACCA CAGACACCGC
 6201 CGAAGCAGAT TCGGGCAGCT TGAAGAACAC CTTCAACAAA GAAGCGGTGC
 6251 AAAGTGAACT GGATTTACAA AGAACCGTCA GCCAAGATTT TAGTAAAAAT
 6301 GTTCAACAAG CCAATACCGA GATTAACCAA CATTTAGACA AACTCAAAGC
 6351 AGACAAAGAA GCAGCCGAAA CAGCAGCAGC CGAGGCATTA GCCAATGGCG
 6401 ATATGGAAC TGCCAAACGC AAAGCCCATG AAGCTCAAGA TGCGGCAGCA
 6451 AAAGCAGATA ATTGGCAACA AGGCAAAGTC ATTCTCAACA TGTTAGCCTC
 6501 AGGTTTAGCT GCGCCGACCC AAAGCGGAGC GGGCATCGCT GCGGCTACCG
 6551 CATCGCCAGC CGTATCGTAT GCGATTGGAC AGCACTTTAA AGATTTAGCC
 6601 GGTCAAAACG CGAATGGTAA ACTAACCGCC AGTCAAGAAA CCGCACACGT
 6651 TCTTGCCAC GCGGTATTAG GAGCAGCGGT TGCCGCAGTA GGAGACAACA
 6701 ATGCTTAGC AGGAGCATTG AGTGCGGGCG GGTGGAAGC GGCTGCGCCT
 6751 TACATCAGCA AATGGTTATA CGGCAAAGAA AAAGGAAGCG ACTTAACGGC
 6801 GGAAGAGAAA GAGACTGTAA CAGCGATTAC AAATGTATTG GGTACGGCTA
 6851 CGGGTGCGGC AGTCGGCAAC AGCGCAACAG ATGCAGCGCA AGGCAGCCTG
 6901 AATGCGCAAA GTGCGGTGGA GAATAATGAT ACTGTAGAGC AAGTGAAATT
 6951 TGCTCTTAGG CACCCTAGAA TTGCTATTGC AATTGGATCT GTACATAAAG
 7001 ATCTTGCTC TACATTAGAG CCTAATATTT CAACAATTGC TTCAACTTTT
 7051 CAATTAAATT TATTTCTTAA TAGTGAATTT GGTGGTGAAG GTGGAGTTGG
 7101 CAATGCATTC AGGCACGTTT TATGGCAAGC AACCATCACA CGAGAATTTG
 7151 GCAAAGATAT TGCTGTTAAA GTAGGAAATA GTCATGAAAG TGGGGAAAAA
 7201 ATTAATTATT CTATAAGACG TAATCTTTCA TTAGATAAAG CAGATGAAAT
 7251 GATTGATCAA CTAAATAACG AAATAGGAAG AGAAATAGCA TTAAATACCA
 7301 ATAGGTTAAA CACAAAAGAG TTAGTTGGAT TAATTCTGGA AACTTATAAA
 7351 AATAATGGTT TTTATCAAGC AGAAAGAAAC AGTAATGGAA ATTATGATGT
 7401 TGTAAGAAAA AGATTATCTG AAAAAGATTA CCAGAAATACA AGCAATATAT
 7451 TGATTCACTT AGATAATACT GGTGCCCGAT TTAAATTC A GCAGAGGAGA
 7501 AAACAAATCA GAGCACAAAT TTCAGCCAGA CAATGGAGAA GATAA

This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

m563.pep..

1 MNKTLRVIF NRKRAVVAV AETTKREGKS CADSDSGSAH VKSVFPFGTTH
 51 APVCRSNIFS FSLLGFSLCL AVGTANIAFA DGIIADKAAP KTQQATILQT
 101 GNGIPQVNIQ TPTSAGVSVN QYAQFDVGNR GAILNNSRSN TQTQLGGWIQ
 151 GNPWLARGEA RVVQNQINSS HSSQMNGYIE VGGRRAEVVI ANPAGIAVNG
 201 GGFINASRAT LTTGQFPQYA GDLSGFKIRQ GNVVIAGHGL DARDTDFTRI
 251 LSYHISKIDAP VWGQDVRVVA GQNDVVATGN AHSPILNNA ANTNNNTANN
 301 GTHIPLFAID TGKLGMYAN KITLISTAEQ AGIRNQQLF ASSGNVAIDA
 351 NGRLVNSGTM AAANAKDTDN TAEHKVNIRS QGVNSGTAV SQQGTQIHSQ
 401 SIQNTGTLIS SGEILIHNSG SLKNETSGTI EAARLAIDTD TLNNQKLSQ
 451 TGSQKLHIDA QGKMDNRGRM GLQDTAPTAS NGSSNQTGNS YNASFHSST
 501 TPTTATGTGT ATVSISNITA PTFADGTIRT HGALDNSGSI IANGQTDVSA
 551 QQGLNNAGQI DIHQLNAKGS AFDNHNGTII SDAVHIQAGS LNNQNGNITT
 601 RQQLIEITDQ LDNAHGKLLS AEIADLAVSG SLNNQNGEIA TNQQLIHDG
 651 QQSTAVIDNT NGTIQSGRDV AIQAKSLSNN GTLAADNKLD IALQDDFYVE
 701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT
 751 DIGTQHNLTN RGLIDGQOTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD
 801 ENGTGAALIA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK
 851 AQRHINAGAT IEAAGKMLRG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
 901 RHELLREGTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
 951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
 1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEBITR NISLGSFAYE
 1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKG
 1101 LVETDPRFAN YRQWLGS DYM LDSLKLD PNN LHKRLGDGYY EQRLINEQIA
 1151 ELTGHRRLDG YQNDEEQFKA LMDNGATAAR SMNLVSGIAL SAEQVAQLTS
 1201 DIVWLVOKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
 1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQSAVTAT QDINNIGGML
 1301 SAEQTLNNA GNNINSQSTT ASSQNTQSS TYLDRMAGIY ITGKEKGVLA
 1351 AQAGKDINII AGQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN
 1401 HVIRGSTNEV GSSIQTGKDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
 1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
 1501 VLQAGNDANI LGSNVIDSNG TQIQAGNHVR IGTQTQSQS ETVHTQKSG

855

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1551 LMSAGIGFTI GSKTNTQENQ SOSNEHTGST VGSLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNST TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVGQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVVISITY GEQQNRQTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKSGS WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKGG
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLGADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQOGKV ILNMLASGLA APTQSGAGIA AATASPAVS Y AIGQHFKDLA
2201 GQNANGKLTA SQETAHVLAH AVLGA AVAAV GDMNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTATITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VHDPGSTLE PNISTIATF
2351 QLNLFNPSEF GEGGVGNF RHVLWQATIT REFGKDIKVK VGNSHESGEK
2401 INYSIRRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILIHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563.pep      MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
              |||||
m563.pep      MNKTLYRVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563.pep      FSALGFSLCLALGTVNIAFADGIITDKAAPKTQQATILQTGNGIPIQVNIQTPTSAGVSVN
              |||||
m563.pep      FSLLGFSCLAVGTANIAFADGI IADKAAPKTQQATILQTGNGIPIQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVVIAGHGL
              |||||
m563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVVIAGHGL
              190     200     210     220     230     240

              240
g563.pep      DARDTDFTRIL-----
              |||||
m563.pep      DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPILNNAANTSNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563.pep      -----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              :|||
m563.pep      GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

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g563.pep      AAANVQDMNNTAEHKVNIRSQA FENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----
               |||::| :||| ||||| |||: ||||| ||||| ||||| ||||| |||:|
m563.pep      AAANAKDTDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLLSSGEILIHNSG
               370      380      390      400      410      420

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g563.pep -----

m563.pep SLKNETSGTIEAARLAIDTDTLNNQKLSQTGSQKLHIDAQGKMDNRGRMGLQDTAPTAS

430 440 450 460 470 480

g563.pep -----

m563.pep NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSIISNITAPTADGTIRTHGALDNSGSI

490 500 510 520 530 540

g563.pep -----
m563.pep IANGQTDVSAQQGLNNAGQIDIHQLNAKGSAFDNHNGTIISDAVHIQAGSLNNQNGNITT
550 560 570 580 590 600

```

                                350      360      370      380
g563.pep  -----EDLAVSGSLNNQNGEATNQQLI IHDGQQSTVVIDNT
                                |||||
m563.pep  RQQLEIETDQLDNAHGKLLSAEITADLAVSGSLNNQNGEATNQQLI IHDGQQSTAVIDNT
                                610      620      630      640      650      660

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          390      400      410      420      430      440
g563.pep    NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS
             |||||
m563.pep    NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS
             |||||
          670      680      690      700      710      720

```

```

              450      460      470      480      490      500
g563.pep      HTLQAGKRIRIKANNLNDNAVQGNIQSGGTTDIGNTQHNLTNRGLIDGQQTKEIQAGQMNNIG
              |||||
m563.pep      HTLQAGKRIRIKANNLNDNAAGNINQSGGTTDIGNTQHNLTNRGLIDGQQTKEIQAGQMNNIG
              730      740      750      760      770      780

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                    510      520      530      540      550      560
g563.pep      TGRIYGDNIAIAATRLDNQDENG TGAAIAAREN LNLGIEQLNNRENSLIYSGNDMAVGGA
               |||||
m563.pep      TGRIYGDNIAIAATRLDNQDENG TGAAIAAREN LNLGIGQLNNRENSLIYSGNDMAVGGA
               |||||
                    790      800      810      820      830      840

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                    570      580      590      600      610      620
g563.pep      LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG
               |||||
m563.pep      LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG
               |||||
                    850      860      870      880      890      900

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	630	640	650	660	670	680
g563.pep	RHELLREGTQHELGFVYNNESDHLRTPDGV	AHENNWKYDYEKVTQETQVTGTAPAKIIA				
		:				
m563.pep	RHELLREGTQHELGWSVYNDES	DHLRTPDGA	AHENNWKYDYEKVTQKTQVTQTAPAKIIS			
	910	920	930	940	950	960
	690	700	710	720	730	740

m563.pep	LMSAGIGFTIGSKTNTQENQSQSNEHTGSTVGS	1560	1570	1580	1590	1600	1610
		1350	1360	1370	1380	1390	1400
g563.pep	LISTQSMDIGAAQNQLNSKTTQT						
	TYEQKGLTVGIQFARYRFGTSDCRSTQSSKQVGQSKN						
m563.pep	TIYAQSIDIQAAHNKLNSTTTQT						
	TYEQKGLTVAFSSPVTDLAQQA- IAVAQSSKQVGQSKN						
		1620	1630	1640	1650	1660	
		1410	1420	1430	1440	1450	1460
g563.pep	DRVNAAAAANAGWQAYQTGKGAQNLANGTTNAKQVSISITYGEQQNRQTTQVQANQAQAS						
m563.pep	DRVNAAAAANAGWQAYQTGKSAQNLANGTTNAKQVSISITYGEQQNRQTTQVQANQAQAS						
		1670	1680	1690	1700	1710	1720
		1470	1480	1490	1500	1510	1520
g563.pep	QIQAGGKTTLYCRRCGEQSNINITGSGVSGRAGTGLIADKQIHLSAEQSNTERSQNKSA						
m563.pep	QIQAGGKTTLIATGAAEQSNINIAQSDVAGKAGTILIADNDITLQSAEQSNTERGQNKSA						
		1730	1740	1750	1760	1770	1780
		1530	1540	1550	1560	1570	1580
g563.pep	GWNAGAAVSFGQGGWSLGVAAAGNVGKGYGDSVTHRSHSHIGDKGSQTLIQSGGDTTIK						
m563.pep	GWNAGAAVSFGQGGWSLGVTAGGNVKGYGNGDSITHRSHSHIGDKGSQTLIQSGGDTTIK						
		1790	1800	1810	1820	1830	1840
		1590	1600	1610	1620	1630	1640
g563.pep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONAGAQVTVGYGFSASGDYSQSKIRADHA						
m563.pep	GAQVRGKGVQVNAKNLSIQSVQDRETYQSKQONASAQVTVGYGFSAGGDYSQSKIRADHV						
		1850	1860	1870	1880	1890	1900
		1650	1660	1670	1680	1690	1700
g563.pep	SVTEQSGIYAGEDGYQIKVGNHTGLKGGIITSSQSAKDKGKNRFSTGTLAGSDIQNYSQY						
m563.pep	SVTEQSGIYAGEDGYQIKVGNHTDLKGGIITSTQSAEDKGKNRFQTATLTHSDIKNHSQY						
		1910	1920	1930	1940	1950	1960
		1710	1720	1730	1740	1750	1760
g563.pep	EGKSFGLGASVAVSGKTLGQGAKNKPQDKHLTSIADKNGASSSVGYGSDSDSQSSITKSG						
m563.pep	KGESFGLGASASISGKTLGQGAQNKPNKHLTSVADKNSASSSVGYGSDSDSQSSITKSG						
		1970	1980	1990	2000	2010	2020
		1770	1780	1790	1800	1810	1820
g563.pep	INTPKNIQITDEAAQIRLTGKIAAQTKADIDTNVTTDTAERHSGSLKNIQFDKDRVQSELD						
m563.pep	INT-RNIQITDEAAQIRLTGKTAQTKADIDTNVTTDTAERHSGSLKNTFNKEAVQSELD						
		2030	2040	2050	2060	2070	2080
		1830	1840	1850	1860	1870	1880
g563.pep	LQRTVSQDFSKNVQQNTNTEINQHLDKLDKADKEAAETAAAEALANGDMETAKRKAHEAQDA						
m563.pep	LQRTVSQDFSKNVQQANTEINQHLDKLDKADKEAAETAAAEALANGDMETAKRKAHEAQDA						
		2090	2100	2110	2120	2130	2140
		1890	1900	1910	1920	1930	1940
g563.pep	AAKADNWQQGKVILNMLASGLAEPTQSGAGIAAATASPDVSYAIGQHFCDLAGQNANGKL						
m563.pep	AAKADNWQQGKVILNMLASGLAAPTQSGAGIAAATASPAVSYAIGQHFCDLAGQNANGKL						
		2150	2160	2170	2180	2190	2200

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGSLSNAE					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSDLTAE					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFQTASDFASSFSYPINMX					
m563 . pep	EKETVTAITNVLTATGA AVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIATAI					
	2270	2280	2290	2300	2310	2320

m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGGVGNAFRHLVWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564 . seq
1   ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAAATGATA TTGCGGGCTT TGCGGGTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTT
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTGGTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAACCTGA ATGGCTATAT TGAAGTGGGC GGACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAAATCG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCTG
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGTGAGGGT
1051 AAATGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCATTTCAT GCCCGCAATG TTCATAATAG CCGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTAA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAATCCCG TTTCACCTAC AGCACCTGCA AAAAATACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAATTGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACACG ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT CAAACCGGCA AGATTGATAA CCGTGAACGT
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTCTGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGG
1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAACGGC AAACCTCTAT CTGCAAAACA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

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2251	ATTCACGATA	AAAATCAAAA	CACTTTGGCG	TTAAACAATG	CGGATGGCAC
2301	GATTCATCT	GCCGGTAATG	TATCGCTACA	AGCCAAATCA	CTCGCCAACA
2351	ATGGCACATT	AACAGCCGGT	AACAAACTGG	ATATTGCTTT	GACGGACGAT
2401	TTCGTCGTAG	AGCGCGACCT	CACTGCAGGC	AAACAATTAA	ATCTAAGCAT
2451	AAAAGGCCGT	CTGAAAAATA	CCCATACCCT	ACAAGCAGGC	CATACGCTCA
2501	AACTCAATGC	CGGCAATATA	GATAACCAAG	TTACAGGCAA	AATTATTGGT
2551	GGAGAACAAA	CGGACATCAC	ATCCGAACAG	CATGTTGACA	ACAGGGGCTT
2601	CTGCAACAGC	GACGGTTTGA	CCCACATCGG	TGCAGGTCAA	ACCCTGACCA
2651	ACACCGGGAC	AGGCAAAATC	TATGGCAACC	ATATTGCCCT	GGACGCGCAA
2701	ATACTGCTTA	ACCGGGAAGA	AACGACGGAA	GGCAGTACCA	AAGCGGGGGC
2751	AATAGCTGCA	AGGAAACGTT	TGGATATTGG	AGCGAAAGAG	ATTCATAACC
2801	AAGAAGGTGC	CCTACTATCC	AGCGAAGGTA	TTTTTGCCGT	AgGTAATCGA
2851	CTGGATGAAC	AACATCATGC	GGCAGGCATG	GCCGATACCT	TTGTTAATGG
2901	CAGTGCCGGT	TTGGAAGTAC	AAGGTGATGC	ATTGATGTCC	GTTCCGAATA
2951	TGCAGAATAT	CAATAATCAC	TTTAAACAG	AGACATACTT	AGCCAAAGCG
3001	GAAAAGCAAG	TCCGCGACTA	CACCGTACTG	GGGCAAAATA	CCTACTATCA
3051	GGCGGGAAAA	GACGGTTTAT	TCGACAACCT	GCAAGGACAA	AAAGACCAAA
3101	CTACTGCTAC	GTTCCATTTA	AAAAATGGTT	CTCGTATTGA	GGCCAAACAA
3151	TGGCATGTCC	GAGACTACCA	CATCGAGACT	TATAAAGAAC	GCATCATCGA
3201	AAACCGGCCG	GCACACATTA	CTGTGGGCGG	TGATTTGACT	GCCTCAGGTC
3251	AAAATTGGCT	GAACAAAGAC	AGCCGGATTG	TAGTAGGCGG	GCGTATTATC
3301	ACTGATGATT	TAAACCAGAA	AGAAATTACC	AATCAAAGTA	CAACAGGCAA
3351	AGTTCGCACA	GATGCTGTGC	GCACACAGTG	GGATTTCAGT	ACAAAAAAG
3401	GATGGTACAG	CGGTAGAAAA	AGACAACGCC	GTAAGTAAAG	AAACCATACT
3451	CCTTACCATG	ATACCCAAT	ATTTACCCAC	GACTTCGACA	CGCCTGTATC
3501	CGTCATCCAA	CAGAATGCCG	CCTCCCTTTC	CTTTCAACCC	GCCGCATCTG
3551	CAATCAAAC	GATTGACGGA	GTATCCACGG	CAGCCGTC	GGTTCAGCGC
3601	ATCCATACCG	GTAATGTGGT	CTCGTTAAAT	AACGCTACTG	TTACTCTGCC
3651	TAACAGCAGC	CTCTATACCA	CCCATCCTGA	CAATAAAGGC	TGGTTGGTTG
3701	AAACCGATCC	TCAATTTGCA	GACTACCGCC	GCTGGTTGGG	CAGCGACTAC
3751	ATGTTGCAAC	AACTGCAATT	GGACACCAAT	CATCTACACA	AACGGCTTGG
3801	CGACGGCTAC	TACGAACAAA	AACTTGTTAA	TGAACAAATC	CATCAGTTAA
3851	CAGGCTACCG	CCGACTCGAC	GGCTACAGGA	GTGATGAAGA	ACAATTCAAA
3901	GCTCTGATGG	ACAACGGCCT	TACTGCTGCC	AAAACATTCT	GTCTCACCCC
3951	AGGTATCGCC	TTGAGTGCAG	AGCAAGTTGC	CCGCTTAACT	TCAGATATCG
4001	TTTGGATGGA	AAATCAAACC	GTACCCCTGT	CTGACGGTTC	GACTCAAACC
4051	GTACTGGTTC	CTAAAGTCTA	TGCCCTGGCG	CGCAAAGGTG	ATCTCAATAC
4101	CTCCGGTGGC	CTGATTAGTG	CCGAACAAGT	CTTACTTAA	CTGCAAAACG
4151	GCAACCTGAC	TAACAGCGGT	ACCATTGCGG	GGCGACAGGC	CGTACTCATC
4201	CAGGCACGGA	ATATTAACAG	CAACGGTAAC	ATTCAAGCCG	ACCAAATCGG
4251	CTTAAAGCT	GAAAAAAGTA	TCAATATCGA	CGGCGGGCAG	GTACAAGCAG
4301	GCAGACTGCT	GACTGCCCAA	CGGCAAAATA	TCAACCTTAA	CGGTACAACC
4351	CAAACTTCCG	GTAATGAACG	TAACGGCAAT	ACCGCCATCG	ATCGTATGGC
4401	CGGCATTAAC	GTGGTTCGGAA	GCCATACTGA	ACAAGTAGAT	AACAGAACTT
4451	CAGACGGCAT	CCTATCCCTG	CATGCCAGCA	ACGATATCAA	CCTCAATGCG
4501	GCCACCGTCT	CTAACCAAGT	TAAAGACGGC	ACTACCCAAA	TTACCGCCGG
4551	CAATAATCTC	AACCTCGGCA	CCATCCGTAC	CGAACATCGC	GAAGCCTATG
4601	GTACATTAGA	TGACGAGAAC	CATCGCCATG	TCCGCCAAAG	TACCGAAGTC
4651	GGCAGCAGTA	TCCGCACGCA	AAACGGCGCA	CTGCTTAGAG	CCGGTAACGA
4701	CTTAAAAATC	CGCCAAGGCG	AACTGGAGGC	CGAAGAAGGC	AAAACCGTCC
4751	TTGCCGCGAG	ACGTGATGTC	ACTATCAGCG	AAGGACGCCA	AATAACCGAA
4801	CTGGATACCT	CGGTAAGCGG	AAAAAGCAAA	GGCATCCTTT	CCAGTACCAA
4851	AACACACGAC	CGCTACCGCT	TCAGTCATGA	TGAAGCAGTC	GGCAGCAACA
4901	TCGGCGGCGG	CAAAATGATT	GTTGCAGCCG	GGCAGGATAT	CAATGTACGC
4951	GGCAGCAACC	TTATTTCTGA	TAAGGGCATT	GTTTTAAAG	CAGGACACGA
5001	CATCGATATT	TCTACTGCCC	ATAATCGCTA	TACCGGCAAT	GAATACCACG
5051	AGAGCAAAAA	ATCAGGCGTC	ATGGGTACTG	GCGGATTGGG	CTTTACTATC
5101	GGTAACCGGA	AAACTACCGA	TGACACTGAT	CGTACCAATA	TTGTCCATAC
5151	AGGCAGCATT	ATAGGCAGCC	TGAATGGAGA	CACCGTTACA	GTTGCAGGAA
5201	ACCGCTACCG	ACAAACCGGC	AGTACCGTCT	CCAGCCCCGA	GGGGCGCAAT
5251	ACCGTCACAG	CCAAAAGCAT	AGATGTAGAG	TTCGCAAACA	ACCGGTATGC
5301	CAGTGAATAC	GCCCATACCC	AGGAACAAAA	AGGCCTTACC	GTCCGCCCTCA
5351	ATGTCCCGGT	TGTCCAAAGT	GCACAAAAC	TCATACAAGC	AGCCCAAAAT
5401	GTGGGCAAAA	GTAATAATAA	ACGCGTTAAT	GCCATGGCTG	CAGCCAATGC
5451	TGCATGGCAG	AGTTATCAAG	CAACCAACA	AATGCAACAA	TTTGCTCCAA
5501	GCAGCAGTGC	GGGACAAGGT	CAAAACAACA	ATCAAAGCCC	CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
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5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
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6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCG CATCGACACC
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7651 ACCGGCAGCG ATCCCTTATT GCGGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1 MNRTLYKVVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51 IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW QGDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNPVSVIPQ IPSTATGSGS STVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHD LAVNTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901	ILLNREETTE	GSTKAGAI	AA	RKRLDIGAKE	IHNQEGALLS	SEGI	FAVGNR
951	LDEQHHAAGM	ADTFVNGS	SAG	LEVQGDALMS	VRNMQNNH	FKTETY	LAKA
1001	EKQVRDYTVL	GQNTYYQAGK		DGLFDNSQOQ	KDQTTATFHL	KNGSR	IEANQ
1051	WHVRDYHIET	YKERIENRP		AHITVGGDLT	ASGQNLNKL	SRIVVGGRI	I
1101	TDDLNDQKEIT	NQSTTGKGR	T	DAVGTQWDSV	TKKGWYSGRK	RQRRTERNHT	
1151	PYHDTQLFTH	DFDTPVSVIQ		QNAASPSFQP	AASAIKLIDG	VSTA	AVNGQR
1201	IHTGNVSLN	NATVTLPNSS		LYTTHPDNKG	WLVEDPQFA	DYRRWL	GSDY
1251	MLQQLQLD	LTNHLHKLRLG	DGY	YEQKLVNEQI	HQLTGYRRLD	GYRSDEEQFK	
1301	ALMDNGLTAA	KTFGLTPGIA		LSAEQVART	SDIVWMENQT	VTLSDEESTQT	
1351	VLVPKVYALA	RKGDNLNTSGG		LISAEQVLLK	LQGNLNTNSG	TIAGRQAVLI	
1401	QARNINSNGN	IQADQIGLKA		EKSINIDGGQ	VQAGRLLTAQ	AQNINLNGTT	
1451	QTSGNERNGN	TAIDRMAGIN		VVGSHTEQVD	NRTSDGILSL	HASNDINLNA	
1501	ATVSNSQVKD	TTQITAGNNL		NLGTIRTEHR	EAYGTLD	DDENHRHVR	QSTEV
1551	GSSIRTQNGA	LIRAGNDLKI		ROGELEAEEG	KTVLAAGRDV	TI	SEGRQITE
1601	LDTSVSGKSK	GLLSSTKTHD		RYRFSHDEAV	GSNIGGGKMI	VAAGQD	INVR
1651	GSNLISDKGI	VLKAGHDIDI		STAHNRYTGN	EYHESKKSGV	MGTGGLGFTI	
1701	GNRKTTDDTD	RTNIVHTGSI		IGSLNGDVT	VAGNRYRQTG	STVSSPEGRN	
1751	TVTAKSIDVE	FANNRYATDY		AHTQEQKGLT	VALNVFPVQ	AQNFIAQAQ	PN
1801	VGKSKNRKVN	AMAAANA	AWQ	SYQATQOMQO	FAPSSSAGQ	QNNNQSPSIS	
1851	VSITYGEQKS	RNEQKRHYTE		AAASQIIGKG	QTTLAATGSG	EQSNINITGS	
1901	DVIGHAGTAL	IADNHIRLQS		AKQDGESEQSK	NKSSGWNAGV	AVKIGNGIRF	
1951	GITAGGNIGK	GKEQGGSTTH		RHTHVGSTTG	KTTIRSGGSDT	TLKGVSOLIGK	
2001	GIQADTRNLH	IESVQDTEY		QSKQONGNVQ	VTVGYGFSAS	GSYRQSKVKA	
2051	DHASVTGQSG	IYAGEDGYQI		KVRDNTDLKG	GIITSSQSAS	DKGKNLFTQTA	
2101	TLTASDIQNH	SRYEGRSFGI		GGSFDLNGGW	DGTVTDKQGR	PTDRISPAAG	
2151	YGSDDGDSKNS	TTRSGVNTHN		IHITDEAGQL	ARTGRTAKET	EARIYTGIDT	
2201	ETADQSGSHL	KNSFDKDAVN		KEINLQREVT	KEFGRNAAQA	VAAVADKLG	N
2251	TSQSYERYQEA	RLTLEAELON		TDSEAEKAAF	RASLGQVNA	LAENQSR	YDT
2301	WKEGGIGRSI	LHGAAGGLTT		TSLGGILAGG	GTSLAAPYLD	KAAENLGPAG	
2351	KA	AVNALGGA		AIGYATGGSG	GAVVGANVDW	NNRQLHPKEM	
2401	KREVEKREGR	KISSQEAAMR		IRRQILRWVD	KGSDQGYTDQ	SVISLIGMKG	
2451	EDKALGYTWD	YRDYQAGARNPQ		TYNDPKLFEE	YRRQDKPEYR	NLTWLHSGTK	
2501	DTKIRQGERK	NEEFALNVAE		GLTSLVNP	PNRIKVPILAGI	RNLKNIGPTV	
2551	TGSDPLLAGA	GNIRIPANGN		VAKGDRI	PDTALASKGIKHK	DRKDKQLEKK*	

Computer analysis of this amino acid sequence gave the following results:

Homology with fha

m564/fha

ID FHAB BORPE STANDARD; PRT; 3591 AA.

AC P12255;

DT 01-OCT-1989 (REL. 12, CREATED)

DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)

DE FILAMENTOUS HEMAGGLUTININ.

SCORES Init1: 190 Initn: 524 Opt: 594

Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

```
m564      .pep    MNRTLYKVVFNKHRCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
              10       20       30       40       50       60
fhab_borpe MNTNLRLVLFSSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
              10       20       30       40       50
```

```

              70          80          90          100          110          119
m564      .pep  LSLLLG-SALILTSSSATAQGIVADKSAPAAQQQPTILQTGNGIIPQVNIQTPTSAGVSVNQ
              ::::: ::::: ||::: | | | : | | | | | | | | | | | | | | | |
fhab_borpe  WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK
              60          70          80          90          100

```

```

      120      130      140      150      160      170      179
m564 .pep YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSSHSSQLNGYIEV
       : ||:|| |::||| :: :||| : |||| :| :::::: |:| |:||
fhab_borpe FQQFNVANPGVVFNGLTDGVSRRIGGALTKNPNLTR-QASAILAEVTDTSPSRLAGTLEV
      110      120      130      140      150      160

```


864

m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDQQAALGSLAAKGELTVSAARAATVA-EL---KSLDNIS					
			720	730	740	750	760
m564	.pep	820	830	840	850	860	870
		IKGRLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLNSDGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
			770	780	790	800	810
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYNHIALDAQILLNREETTEGSTKAGAI AARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
			820	830	840	850	860
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGIFAVGNRLDEQHHAAAGMADTFVNGSAGLEVQGDALMSVRNMQNNHFKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
			870	880	890	900	910
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLGQNTYYQAGKDLFDNSQGQKQDQTATFHLKNGSRIEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGHELDLGTAAVAVDV---NGTGDVRVAKLVSDAGADLQAGRS					
			930	940	950	960	970
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGRIITDDLNOKE					
fhab_borpe		MTLGIVDTTGDLQARAQQKLELGSVKSDDGLQAAAGGALS LAAAEVAGALELS---GQGV					
			980	990	1000	1010	1020
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRDVGTVQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
			1040	1050	1060	1070	1080
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QONAASPSFQPAASAIKLIDGVSTA AVNGQRIHTGNVSVLNNATVTLPNSSLYT					
fhab_borpe		SVVVRAQGNVTVGRGDEPHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
			1090	1100	1110	1120	1130
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQLDTNHLHKRLGDGYEQLVNEQI HQ					
fhab_borpe		EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRIQIDV					
			1150	1160	1170	1180	1190
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKT FGLTPG-IALSAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI-----TDAVTGEARKDES VVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
			1200	1210	1220	1230	1240

866

		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGEQGGSTTHRHVHGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
		:		:	: : :		: : :
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGHIHG-----DVDNRSV-					
		1870	1880	1890		1900	

		2020	2030	2040	2050	2060	
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE					
		: : :	: :	: :	:	:	
fhab_borpe		VRTVSAMEYFKTFLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY					
		1910	1920	1930	1940	1950	1960

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNHS--RYEGRSFGIGGS					
		: : :	:	: :	:	: : :	: :
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAGEGRKI-FGEY					
		1970	1980	1990		2000	2010

		2130	2140	2150	2160	2170	
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGS DGSKNSTTRSGVNTNHIHITDEAG					
		: : :	: : :	: :	:	: : : : : :	
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRVRHDQLG-----QRYGKALGGMDAETKEVDGIIQ					
		2020	2030	2040	2050	2060	2070

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKEFGRNAA					
		: :	:	: :	: : : :	:	: : :
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGRVT--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEEAFAFRASLGQVNAYL-----					
		: :	: : : :	: : : :	:	:	: :
fhab_borpe		AALGADWRALGHSQMLQWRKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		: : :	:	: : : : :	: :	: :	: :
fhab_borpe		AQNRGRPEGLKIGAHSATS SVGSFDALRDVGLKRLDIDDALAAVLVNPFIHTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccttcggttt cgcacgcgcg aacgacaccg gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaataccttc
201 ttggggcgaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgacg
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTCG CCCGTCCCAG ACCGGCGGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

```


867

```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAAGCGC
351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGT AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCTGCGTGT CCGATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAAGTGC
351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACTCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGT AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSAF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

868

```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSLCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
m565.pep  KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210
a565      KAMANTTSAFNTSSSIANSINTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggtaac
51 ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggtc
151 gccggccttg tgggtgattt ccacgcgttc gccgtcgggtg gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacgggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51 AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51 GGTGTGTTAG CCCGAGTAGC TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATT CCACGCGCTC GCCGTGCGGT GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGCG GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51 AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           10      20      30      40      50      60
           |||||

```

869

```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG AACAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTACCG
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCTTG TGGGTGATT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCGCGCG GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTGAGG TCTCTGCCGA GCGCGCCGCG GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51  ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60
           70      80      90      100     110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq..
1  atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcggtt
51  tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtagcgag
101 caaagagggc ggatacggcg tgttgggtgc gaacgcgcgc gcttgccggc
151 gcggaatcgc agctggtgca ggaaatcgcc cgggaagtgc gtttgaaaaa
201 cgcgctcaag gcagtgccgg aagattacga ctttatcctg atcgactgtc
251 cgccttcgct gacgctgttg acgcttaacg gcttggtggc ggccggcggc
301 gtgattgtgc cgatgttggt cgaatattac gcgctggaag ggatttccga
351 tttgattgcg accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
401 acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctggtt
451 gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
501 aaccgccatc ccgcgcaata tccgccttgc ggaagcgccg agccacggta
551 tgccggtgat ggcttacgac gcgcaggcaa aggggtgcaa ggcgtatctt
601 gccttggcgg acgaactggc ggcgagggtg tcggggaaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAASR RVCSPAFIRS YWAMRTCSRR RYAAKRADTA CWVRTRALAG
51  AEIELVQEIA REVRILKNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDITGIVR TMYDSRSRLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGCGA  ACATCCTTGC  CATCGCCAAT  CAGAAGGGCG  GTGTGGGCAA
51  AACGACGACG  ACGGTAAATT  TGGCGGCTTC  GCTGGCATCG  CGCGGCAAAC
101 GCGTGCTGGT  GGTTCGATTG  GATCCGCAGG  GCAATGCGAC  GACGGGCAGC
151 GGCATCGACA  AGGCGGGTTT  GCAGTCCGGC  GTTTATCAGG  TCTTATTGGG
201 CGATGCGGAC  GTGCAGTCGG  CGGCGGTACG  CAGCAAAGAG  GGCGGATACG
251 CTGTGTTGGG  TGCGAACCGC  GCGCTGGCCG  GCGCGGAAAT  CGAACTGGTG
301 CAGGAAATCG  CCCGGGAAGT  GCGTTTGAAA  AACGCGCTCA  AGGCAGTGGA
351 AGAAGATTAC  GACTTTATCC  TGATCGACTG  CCCGCCTTCG  CTGACGCTGT
401 TGACGCTTAA  CGGGCTGGTG  GCGGCGGGCG  GCGTGATTGT  GCCGATGTTG
451 TGCGAATATT  ACGCGCTGGA  AGGGATTTCC  GATTTGATTG  CGACCGTGCG
501 CAAAATCCGT  CAGGCGGTCA  ATCCCGATT  GGACATCACG  GGCATCGTGC
551 GCACGATGTA  CGACAGCCGC  AGCAGGCTGG  TTGCCGAAGT  CAGCGAACAG
601 TTGCGCAGCC  ATTTCTGGGA  TTTGCTTTTT  GAAACCGTCA  TCCCGCGCAA
651 TATCCGCTT  GCGGAAGCGC  CGAGCCACGG  TATGCCGGTG  ATGGCTTACG
701 ACGCGCAGGC  AAAGGGTACC  AAGGCGTATC  TTGCCTTGGC  GGACGAGCTG
751 GCGGCGAGGG  TGTCGGGGAA  ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN  QKGGVGKTTT  TVNLAASLAS  RGKRVLVVDL  DPQGNATTGS
51  GIDKAGLQSG  VYQVLLGDAD  VQSAAVRSKE  GGYAVLGANR  ALAGAEIELV
101 QEIAREVRLK  NALKA VEEDY  DFILIDCPPS  LTLTLNGLV  AAGGVIVPML
151 CEYYALEGIS  DLIATVRKIR  QAVNPDLDIT  GIVRTMYDSR  SRLVAEVSEQ
201 LRSHFGDLLF  ETVIPRNIRL  AEAPSHGMPV  MAYDAQAKGT  KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

m567.pep      60      70      80      90      100      110      119
GVYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKA VEED
g567          AFIRSYWAMRTCSRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKA VEED
                20      30      40      50      60      70

m567.pep      120      130      140      150      160      170      179
YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
g567          YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
                80      90      100      110      120      130

m567.pep      180      190      200      210      220      230      239
TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
g567          TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETAIPRNIRLAEAPSHGMPVMAYDAQAKG
                140      150      160      170      180      190

m567.pep      240      250
TKAYLALADELAARVSGKX
g567          AKAYLALADELAARVSGKX
                200      210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGCGA  ACATCCTTGC  CATCGCCAAT  CAGAAGGGCG  GTGTGGGCAA
51  AACGACGACG  ACGGTAAATT  TGGCGGCTTC  GCTGGCATCG  CGCGGCAAAC
101 GCGTGCTGGT  GGTTCGATTG  GATCCGCAGG  GCAATGCGAC  GACGGGCAGC
151 GGCATCGACA  AGGCGAGTTT  GCAGTCCGGC  GTTTATCAGG  TCTTATTGGG
201 CGATGCGGAC  GTGAAATCGG  CGGCGGTACG  CAGCAAAGAG  GGCGGATACG
```

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```

251 GCGTGTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACCGGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTTCGGGA TTTGCTGTTT GAAACCGTCA TCCCCGCGAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

```

m567/a567 97.7% identity in 257 aa overlap

```

              10      20      30      40      50      60
m567.pep      MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
a567           MSANILAIANQKGGVGKTTTTVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
              10      20      30      40      50      60

              70      80      90     100     110     120
m567.pep      VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
a567           VYQVLLGDADVQSAAVRSKEGGYVGLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
              70      80      90     100     110     120

              130     140     150     160     170     180
m567.pep      DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
a567           DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
              130     140     150     160     170     180

              190     200     210     220     230     240
m567.pep      GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
a567           GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
              190     200     210     220     230     240

              250
m567.pep      KAYLALADELAARVSGKX
a567           KAYLALADELMARVSGKX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
 51 gataccttgc agaatctgcc gattaaagcg ttcgcggctg cccaatattt
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaca gccccatcag gaacgaaact tcgtcttcgg ggcgacgcca
201 gttttcgggt gaaaaggcaa acacggtcag atattgcacg ccagtttg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```

q568.pap

```

1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

```

m568.seq

1	ATGCTCAGGG	TCAGGCCGGT	ATTGTTTGCC	GTCAACGCTT	CCGCCTCTTC
51	GATGCCTTGC	AGAATCTGCC	GGTTGAAGCG	TTCGCGGCTG	CCCAATATCT
101	TCAGGCGCAT	ATTGTTTTTCG	TGCAGGCGCG	GTACCTGTTT	TTGCAAAGCC
151	TGTA AAAACA	GCCCCATCAG	GAACGAAACT	TCGCTCTCGG	GGCGCGCCCA
201	GTTTTCGGTT	GA AAAAGCAA	ACACGGTCAG	ATATTGCACA	CCCAGTTTGG
251	CGCAATGCTT	CACCATATTT	TCCAATGCGT	CCAAACCGCG	TTTGTGTCCC
301	ATTATGCGCG	GGAGGAAACG	TTTTTTCGCC	CAACGGCCGT	TGCCGTCCAT
351	AATCACGGCG	ATATGCTTGG	GAATGCGGTT	GTGTTCCAAA	ACGGCCTGCG
401	TGCTGCTTTT	CATGTCTGCC	TTTCGCGGTT	CGGCATTTCAA	ATGCCGTCGT
451	AACGCCGAAC	CGTGCGGTT	AAATTGCCAT	CAAACTTTCT	TCTTTGGCAG
501	TCAGGAGTTT	GTCGGCTTCG	GTAATGTATT	TGTCGGTCAG	TTTTTGAACC
551	GCTTCTTCGC	CGCGACGTGC	CTCGTCTTCG	GAAATTTCTT	TGTCTTTGAG
601	GAGTTTTTTT	ATGTGGTCGT	TGGCATCGCG	GCGCACGTTG	CGGATAGAGA
651	CGCGGCTTCG	TTCCGCTTCG	CCGCGTACGA	CTTTAATCAG	GTCTTTGCGG
701	CGTTCCTCGG	TCAGCATGGG	CACGGCAGC	CGGATCAGGT	CGCCGACAGC
751	TGCGGGGTTT	AGTCCCAAGT	TTGA		

m568.pap..

1	MLRVRPVLFA	VNASASSMPC	RICRLKRSRL	PNIFRRILFS	CRRRTCFCKA
51	CKNSPIRNET	SSSGRRQFV	EKANTRYCT	PSLAQCFTIF	SNASKPRLCP
101	IMRGRKRFFA	QRPLPSIITA	<u>ICLGMVCSK</u>	<u>TACVLLFMSA</u>	FRSGAFKCLR
151	NAEPCRLNCH	QIFFFGSQEF	<u>VGFGNVFVGQ</u>	<u>FLNRFFAATC</u>	LVFGNFFVFE
201	EFFDVVVGIA	AHVADRDAAF	FRFAAYDFNQ	VFAAFLGQHG	HRHADQVADS
251	CRVOSOV*				

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMP	CRICRLKRSRLPNIFRR	ILFSCRRRTCFC	KACKNSPI	RNET	
	:	:	:	:	:	
g568	MLRVRPVLFAVKASASSI	PCRICRLKRSRLPNIFRR	ILFSCRRRTCFC	KACKNSPI	RNET	
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRY	CTPSLAQCFTIFSNASK	PRLCPIMRGRKRFFA	QRPLPSIITA		
	:	:	:	:	:	
g568	SSSGRRQFSVEKANTVRY	CTPSLAQCFTIFSNASK	PRLCPIIRGRKRFFA	QRPLPSIITA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMS	AFRGSAPFKRLNAEPC	RLNCHQIFFFGSQE	FVGFGNVFGQ		
	: :	: :	: :	: :	: :	:
g568	MCLGMVCSKMCVLLFIS	AFRGSAPFKRLNAAPX				
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFF	VFEFFDVVGIAAHVAD	RDAAFFRFAAYDFNO	VFAAFLGOHG		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTGAC  GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTCG  TGCAGGCGG GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CGGCATTCAA ATGCCGTCTG
451 AACCCGAAC CGTGCAGGT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTCG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLRNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVGIA AHVADGDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

m568.pep	10	20	30	40	50	60
a568	10	20	30	40	50	60
m568.pep	70	80	90	100	110	120
a568	70	80	90	100	110	120
m568.pep	130	140	150	160	170	180
a568	130	140	150	160	170	180
m568.pep	190	200	210	220	230	240
a568	190	200	210	220	230	240
m568.pep	250					
a568	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttggtttggt tatgttgttt
251 tggcattttg gctcgccgtt atgcctttgt gggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccttggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTC AACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTCT ACCGTGTGCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GCGCGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCCGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLI GLVL TVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSL
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
	10	20	30	40	50	60
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
	70	80	90	100	110	120
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLMPFWF					
	130	140	150	160	170	180
m569.pep	ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
	130					
g569	ALVSLAPASRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGCGGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```



```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTAACGCGC GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTGTGCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GGCGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAEFLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLI GLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRDTSI
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

```

              10      20      30      40      50      60
m569.pep    MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
              |||
a569         MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m569.pep    TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLVMPFWF
              |||
a569         TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLVMPFWF
              70      80      90      100     110     120

              130     140     150     160     170     180
m569.pep    ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
              |||
a569         ALVSLRPHPD DALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC
              130     140     150     160     170     180

              190     200     210     220     230     240
m569.pep    VAVYMTAVRSAGWLAFDTGWFDTVLI GLVLT VVSVCGDLL ESWLKRAAGI KDSSKLLPGH
              |||
a569         VAVYMTAVRSAGWLAFDTGWFDTVLI GLVLT VVSVCGDLL ESWLKRAAGI KDSSNLLPGH
              190     200     210     220     230     240

              250     260
m569.pep    GGVFDRDTSLIAVISVYAAMMSVLNX
              |||
a569         GGVFDRDTSLIAVISVYAAMMSVLNX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatecgtt tgaccgcgc gtttgcgcc gccctgatec gtttatgctg
51  caccacaggc gcgcacgccg acaccttcca aaaaatcggc tttatcaaca
101 ccgagcgcgt ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaaggcttg gatttggaaa ggcagctcgc cggcggcaaa cttaggacg
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgttc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtttgcc tccctccagc aaaacgcaa ccgcgtcatc gtcaaatcgc

```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
 451 acccaatagc acgttaccga cagcgtcatt aaagaaatga acgcccgtg
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MTRLTRFAAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
 151 TQYDVTDSVI KEMNAR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRFAAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVYVN
 151 TQYDVTDSVI KEMNAR*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRFAAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDGFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAPRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
 51 CACCGCAGGC GCGCACGCCG ACACCTTCCA AAAAATCGGC TTTATCAACA
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
 151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
 201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
 401 CCAAACAGGA AGGTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570    97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep     MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
              |||||
a570          MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTL DSEFSARQD
              10      20      30      40      50      60

              70      80      90     100     110     120
m570.pep     ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              |||||
a570          ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              70      80      90     100     110     120

              130     140     150     160
m570.pep     SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX
              |||||
a570          SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccgttt tcggcgggcgg
 51  tataggttct gcgcgtccac acgctgcctg cgtcggcaaa cagggtcagg
101  cggacggtgc gtgcgtcttt cgcacgggc atcggaaga gcagctcggc
151  ggagacgttg gctttttgtg tgcgcgcta gctgatttt tcgcgtatt
201  cgtcatacac ttccgggccc agcgtgccgc ttctgtagcc gcgcaccgaa
251  cccaggccgc cgcgtagaaa gttttcaaag aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgct...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRV VTFVGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAAFWA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTGT AACCCCTGCCG CCGGTCGCGG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTTCGCC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG
251  TATCCGCGCA CCGAACCCAG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301  GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACAGGT TTGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTGCTGCCA GGCAGGGCGA TTCGCGCTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAADVFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDGFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVNLNPAAGRGTA VVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
g571      MRVFRVNRVFTVFGGGIGSAVPHAACVKGQAQADGACVFTGHRREEQLGGDVGF
           10      20      30      40      50

      70      80      90     100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
g571      FVAAVADFFAVFVIHFRATERAAAFVAAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           60      70      80      90     100     110

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGSVVLQFAARQDGFVHARQVAARRPX
g571      EGFA
           119

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG CCGGCCCGT AAATGTTTG AACCTGCCG CCGGTCGCGG
51 AACTGCTGTT GTCGTCGTAG GTTTGCCGT CCCACACGCT GCCTGCGTCG
101 GCAAACAGGC TCAGGCGGAC GGTGCGCGC TCTTCGCGC CGGGCATCGG
151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTGCCG CCGTAGCTGA
201 TTTTTTCGCC GTATTCGTCA TACACTTTCG GACCGAGCGT GCCGCTTTCG
251 TATCCGCGCA CCGAACCCAG GCCGCCGCCG TAGAAGTTT CAAAGAAGGG
301 GATTTCTTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351 GCATCAGCGT GAAGTTTTG CTTAAGGGGA AGAACCAGGT TTGGTTGTGG
401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCG GGCAGGGCGA TTTCGGCGTT
451 CACGCCCGTC AGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNVL NPAAGRGTA VVVVGFVAVPHA ACVKGQAQAD GARVFRAGHR
51  EEQLGGDVGF FVAAVADFFA VFVIHFRTER AAFVSAHRTQ AAAVEVFKEG
101 DFFGSAVAAR NADFAAEHQ EGFA*GEEPG LVVGGGVVLQ FAAGQDGFV
151 HARQVAARRP *

```

m571/a571 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m571.pep  MGIAGAVNVNLNPAAGRGTA VVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
a571      MGIAGAVNVNLNPAAGRGTA VVVVGFVAVPHAACVKGQAQADGARVFRAGHREEQLGGDVGF
           10      20      30      40      50      60

      70      80      90     100     110     120
m571.pep  FVAAVADFFAVFVIDFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
a571      FVAAVADFFAVFVIHFRTERAAAFVSAHRTQAAAVEVFKEGDFFGSAVAARNADFAAEHQ
           70      80      90     100     110     120

      130     140     150     160
m571.pep  EGFAQGEEPLVVGGSVVLQFAARQDGFVHARQVAARRPX
a571      EGFAQGEEPLVVGGSVVLQFAAGQDGFVHARQVAARRPX
           130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..

```

1  atgtgcgcca tgcgtcggggc ggcggggctg ccttccgcgc tcgcagcggc
51  gcaaaaagggc aaaaccattt atctggcaaa caaagaaacg ctggtggttt
101 ccggcgcggtt gtttatggaa accgcccgcg caaacggcgc ggcagtgttg
151 cccgtcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 ccggcgggccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 ccggcgagggc cgggtcaaaca cccaattggc cgtatggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggctggt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgata tgcgaacgcc catcgctatc tgtttgggct
551 tgcccgcgagc catcgattcg ggtgtcggca aactcgattt cggcgcatcg
601 tccgcgctga ccttccaaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgcttat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcgcgcaa cgaaaccgcc gtcgcccgtt ttttgacgg acagattaag
751 tttaccgaca ttgccaaaac cgtcgcccac tgtcttgcac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccggacac
851 gcgcacaagc gcgggcatat atcggcacac tgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

g572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAVAL
51  PVDSEHNAIF QVLPDYDTR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFGAL
201 SALTFAQPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```

1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATT TCTGGCAAA CAAAGAAACG CTGGTGGTTT
101 CCGCGCGGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCGGTCGACA GCGAACACAA CGCGTTTTT CAAGTTTTGC CGCGCGATTA
201 CGCGCGCGCT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGCGGGCCC GTTTCTGACC GCGATTAA ACACGTTTCA CCGCATTACG
301 CCGCCCCAAG CGGTCAAACA CCCCATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTCTGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCCGAGC CATCGATTCT GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CTTTCCAAA GCGCGACTTT GACCGCTTCC CCGCTCTGAG
651 GCTGCGCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TGCCTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCT TTTTGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAC CGTCGCCAC TGTCTTGAC AAGACTTTTC
801 AGACGGCATA GGCATATAG GGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGACAAGC GCGAGCATTT ATCGGCACAC TCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```

1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAVAL
51  PVDSEHNAVF QVLPDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFAQPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAVALPVDSEHNAVF
          |||
g572       MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAVALPVDSEHNAIF
          |||

          70      80      90     100     110     120
m572.pep  QVLPDYAGRLENEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||
g572       QVLPDYDTRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS
          |||

```

880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572 . pep	ATMMNKGLELIEAHWLFNCPDPKLEVVHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPDPKLEVVHPQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572 . pep	CLGLPERIDSGVGDLDFDALSALTFFQKPDFRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGKLDGALSALTFFQKPDFRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572 . pep	VAAFLDGGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGGQIKFTDIAKTVAHCLAQDFSNMGDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```
a572 . seq
1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTCTG
151 CCGTTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTCG CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGGCC GTTCTGACC GCCGATTAA ACACGTTTCA CAGCATTACG
301 CCCGACCAAG CGGTCAAACA CCCCAATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC TATCGCTTAT TGTTTGGGTT
551 TGCCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATTG CGACGCATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTTT GACCGCTTCC CCGCGCTGAA
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TGCGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCTT TTTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GGCGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGACAAGC GCGGGCATT ATCGGCACAC TCGCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```
a572 . pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVHP
151 QSVIHSMVRY RDGSLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFFQKPDF DRFPCLLAY EAMNAGGAAP CVLNAANEAA VAAFLDGGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*
```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVL PVDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572 . pep	QVLPDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

881

	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDPKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgccctgtt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaatct cggcagggtc ttccgccgtt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga caccgtctta
251 cccgaacccg tcggaccggt taccagcacc atcccgtaag gacggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaaccg agctggtcga
351 tgttcaaaga cgcggcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaaag gtcagctgca tcctaccgtc ctgcggtatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc ggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac caccctcgcg agctgccgtt ccacacggaa
601 acggatacgc gcatttgtgt cgtaaaactc gaaatggatg tcggatgccc
651 cgctacgcaa ggcacccgac aaagttttat ggataaacct cggaaacaggg
701 cgtctctctc cctcctcgtc gtcgatatac aggggtgtgg tttcctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgatgtcgaa cgcgaacca
801 cccaatcgag caaacccgcc aactggatcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcaga aaccgttttc tgaatttgcg gcattctggg
901 cggatcgga accgcaaaaa ataccttgct gcccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgctcctcgg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgaataac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacacgg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTO ERLQSSGKSQ TLLIIDVNL
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHPVTRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPPFGNVQ TRHYLNPGSK LPPYRNRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPATQ GIRQSFMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTACCAAC aCaw_TTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

```

```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51 DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPFNGVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
g573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHFFLKR LKTELVDVQR					
g573	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVTRVNRFFQQFFLER LKTELVDVQR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPFNGVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFNGVQTRHYLNPGSK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
g573	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVGCPTQGIQSFMDKPRNRAVFCLLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTTRTHPIEQTRQLVILDNDQLNRNPGCRNRFNLRHLG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq
1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAA ATACTTTGTC GCCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep
1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRRNCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNP HH DLFQKRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCFAAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT	DHNDVRVLTQERLQSSGKSQ	ALLIIDVNLI	DARQVNLGRV		
a573	MPCLCRLNRNIGSFQITNLT	DHNDVRVLTQERLQSSGKSQ	ALLIIDVNLI	DARQVNLGRV		
	70	80	90	100	110	120
m573.pep	FRRNCNIYRLRIQNIQTGIER	HRLTRTRRTGYQHHPVGT	VNRYQHFXFLKRLKTELVDVQR			
a573	FRRNCNIYRLRIQNIQTGIER	HRLTRTRRTGYQHHPVGT	VNRYQHFXFLKRLKTELVDVQR			
	130	140	150	160	170	180
m573.pep	RGIGIQNP HH DLFQKRRQC	ADTEIDRLAALLKGQLHP	AVLRYPPFGNVQ	TRHYLNPGSK		
a573	RGIGIQNP HH DLFQKRRQC	ADTEIDRLAALLKGQLHP	AVLRYPPFGNVQ	TRHYLNPGSK		
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHT	ETDTGIVFVKLEMDVRC	FAAQGIRQSLMDKPR	NRRAVFCLLV		
a573	LPPYRNGRLNHLAELPVHT	ETDTGIVFVKLEMDVRC	FAAQGIRQSLMDKPR	NRRAVFCLLV		
	250	260	270	280	290	300
m573.pep	VDIQGVAFLLPLPKLLKQ	RCRTTRTHPIEQTRQLVILD	NNDQLNLNPGCR	NGFLNLRHLC		
a573	VDIQGVAFLLPLPKLLKQ	RCRTTRTHPIEQTRQLVILD	NNDQLNLNPGCR	NGFLNLRHLC		

884

	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggctgggt tgccgcccg cgtgatatga aaaccgtatt gaagcaggca
151 aaaagcatcc ctccgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caacagcggg cgccgggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cgacaatgc tcgattctcc
351 cgatccgtgc ccgcaaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaag cgccgggttg gtcgatcgtg ccgaacagat ttttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgctt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgccgcgcgtc
751 gaagcctatg ccgccatcga gcagcaaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaacc tctgacagga tatatgcaga cgtttcccca acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg cttaaggggc agaaagaagc
951 cgcgcaaaac gccgtcgagc ttgtccgcgc caagccgcac cttaacggcg
1001 tgtaccgcct gctcgggttg aaactcagcg atttggatcc ggcttggaaa
1051 gccgatgccg acatgatgag ttccgttatc ggacggcagc tccagcgagc
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLF LAQNYQSAGL VDRAEQIFLG
151 LQDGEAREAR RQHLNLIYQQ DRDWEKAVET AQLLSHDEQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDI HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLDPFAWK
351 ADADMMSVI GRQLQRSVMY RCRNCHFQSQ VFFWHCPACN KWQTFPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCTGCTGCG CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCTCG GCAAACTTTA CCGCCAGCGT
301 GCGGAAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGAGG GTAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACCTGCCC AAGCGCGCT GTTCAAGTCC AATTCGATG TCGCGCGTTT

```

m574 . pep . .

1	MRPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA
51	KSIPSGFYKS	LDALVDRNSG	RAARELAEVU	DGRPQSYDLN	LTLGLKLYRQR
101	GENDKAINIH	RTMLSDPDTV	GKGRARVLFE	LAQNYSHAGL	VDRAEQIIFLC
151	LQDQGMKARE	RQHLLNIYQQ	DRDWEKAVET	ARLLSHDDQT	YQFEEAQFYG
201	ELAQGAALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE	HQQGNFPAAV
251	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQKG	PEEGLNRLTG	YMQTFPELDL
301	INVVYEKSLI	LKCEKEAAQT	AVELVRRKPD	LNGVYRLLGL	KLSDMNPAAWK
351	ADADMRRSVI	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQTFTPNKI
401	EV*				

m573/g573 97.8% identity in 402 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGCGCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCAGAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCGGCTGTC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAAGCTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCGAC CTCAACGGCG
1001 TGTACGCGCT GCTTGGTTTG AAATCAGCG ATTTGGATCC GGCTTGGAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLTDSPTT GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQAAALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HROGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSDLDPWAK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

m574/a574 97.5% identity in 402 aa overlap

10 20 30 40 50 60
m574.pep MRPNLPNSLKKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a574 MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS
10 20 30 40 50 60

70 80 90 100 110 120
m574.pep LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a574 LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLTDSPTT
70 80 90 100 110 120

130 140 150 160 170 180
m574.pep GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a574 GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET
130 140 150 160 170 180

190 200 210 220 230 240
m574.pep ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDFVARFNVGKALEANKKCTRANMILGDIE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a574 ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE
```

887

	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKPEEGLNRLTGYMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDMNPAWKADADMMSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLNGVYRLLGLKLSDDLPAWKADADMMSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

g575.seq (partial)

```

1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtcaaaca gtccgcttcc ggttctctct tccgcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggaacttc actggtgtgt tccgcaacag
151 gtccggaaac ggtgttaccg gtctcgtcgg tcggcggtgc gatggcagaa
201 gcggcggttt cttggggggg cggattcggc agcggtttcc gatgcggcag
251 tatttgcagc ggttacaggt ccgggttggc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggtcgggt cgaacggccg gttttccgc
351 ttttgcttcg ggcgcggcaa cttttgcttc aggtttttca accggttttt
401 cgacaggttt ctctatcggg ttctccacag ttgcctgttt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttccgccgtt gcggtttggg
501 ttgttccgct ttgatttttt tgggtgctgc cgctttgatc ctgttcagat
551 tcggaatgtg a*
```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

g575.pep (partial)

```

1  ..MPCLRRQAAR CTNRRTDRQT VRFRLLRQK PVRQVRQVR RQLHWLFPQQ
51  VRKRCYRFRR SACRWQKRRL LGGADSAAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSF RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDSG
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

m575.seq..

```

1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTAACGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGC GCTGCCAGGC TGTCGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCTCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATCTTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATTAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGATG GAACGCCGA ACAGACCGTC AAACAGTCC CTTTCGGTTT
701 CTCTTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTCTGAT GGCAGAAGCG GCGGCTTCTT GGGGGCGGGA
801 TTCGGCAGCG GTTTCCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTCCG
851 TTCGAACGGC CGGTTTTCCT GCTTTTGCTT CGGGCGCGGC AACTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTCCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGGTT
1001 GTTCGCTTTT GATCCTGTTC AGATTCCGAA TGTGA
```

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

```
m575.pep
1  MVSGEAEFRK PASPEGEAGF AEAUSSVPIW LFEGRLESEK VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNRPNSNP LSVSSSAETC STGSETALPV
251 SSVGVMAEA AASWGADSA VSDAAVFAAG TSGRTAGFS AFASGAATFA
301 SGFSTGFSTV ACLDGS DGM DAVSALGFAVC GLGCSALILF RFGM*

m575/g575 70.2% identity in 114 aa overlap

                240      250      260      270      280
m575.pep      SSAETCSTGSETALPVSSVGVMAEAAASWGADSAVSDAAVFAAGTG-----
g575          LHWLFPPQVRKRCYRFRRSACRWQKRLLGGADSAVSDAAVFAAGTGPWRSVAEAGVS
                50      60      70      80      90     100

                290      300      309      310      320
m575.pep      -----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSDGMDAVSALGFA
g575          DTAGLGSRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSDGMDAVSALGFA
                110     120     130     140     150     160

                330      340
m575.pep      VCGLGCSALI-----LFRFGMX
g575          VCGLGCSALIFLGAAALILFRFGMX
                170     180
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

```
a575.seq
1  ATGGTTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGCAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGACAA CTCTTCTTCA GATCCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGAGTTT CACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
701 AAACCTGTTC GACAGGTTTC GAAACGGCGT TACCGGTTTC GTCGGTCGGC
751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
801 TTCCGATGCG GCAGTATTTG CAGCGGGTAC AGGTCGGGT CGAACGGCCG
851 GTTTTTCCGC TTTTGCTTCG GGCGCGGCAA CTTTTGCTTC AGGTTTTTCA
901 ACCGGTTTCT CTACCGTTGC CTGTTTGGAC GGTTCGGACG GCATGGATGC
951 GGTTCGGCT TTGGGTTTCG CCGTTTCCGG TTTGGGTTGT TCCGCTTTGA
1001 TCCTGTTCAG ATTCGGAATG TGA
```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

```
a575.pep
1  MVSGEAEFRK PASPEGEAGF AEAUSSVPIW LFEGRLESEK VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSS DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
251 VMAEAAASW GADSAAVSDA AVFAAGTGS RTAGSAFAS GAATFASGFS
301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *
```

889

m575/a575 98.8% identity in 344 aa overlap

m575.pep	10	20	30	40	50	60
	MVSGEAAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEAAFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
m575.pep	70	80	90	100	110	120
	SMTISTGLYGLKVSGSYTSLVDSMAFQASARFWVSSSCVSAPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVSGSYTSLVDSMAFQASARFWVSSSCVSAPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
m575.pep	130	140	150	160	170	180
	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
	130	140	150	160	170	180
m575.pep	190	200	210	220	230	240
	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTDSSVRRARLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
m575.pep	250	260	270	280	290	300
	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMAEAAASWGADSAAVSDAAVFAAGTGSGRTAGFSAFASGAATFA					
	240	250	260	270	280	290
m575.pep	310	320	330	340		
	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1 ..atgggcggtgg acatcgagacg ctccctgaaa caaatgaagg aacaggggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccagggaagt gatgatgaaa
151 ttcttgacg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccc
251 aagacggcgt gaagaccact gcttccgggtc tgcagtacaa aatcaccaaa
301 caggggtgaag gcaaacagcc gacaaaagac gacatcgta cctgtgaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcggg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCGGG GTTGGACCGA AGCGTACAG CTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

	10	20	30	40	50	60
m576.pep	MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	AQEVMKFLO
g576	MGVDIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ	AQEVMKFLO	
	10	20	30	40	50	
	70	80	90	100	110	120
m576.pep	EQQAKAVEKH	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKQPTKDDIV
g576	EQQAKAVEKH	KADAKANKEK	GEAFLENAA	EDGVKTTASG	LQYKITKQGE	GKQPTKDDIV
	60	70	80	90	100	110
	130	140	150	160	170	180
m576.pep	TVEYEGRLID	GTVFDSSKAN	GGPVTFPLSQ	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE
g576	TVEYEGRLID	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE
	120	130	140	150	160	170
	190	200	210	220		
m576.pep	QGAGDKIGPN	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VN	
g576	QGAGEKIGPN	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN	
	180	190	200	210		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCGCCGCG TTCTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCGG TCACCTTCCC TTTGAGCCAA

```



```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVTTSAG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
10 20 30
MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
|||||
a576
30 40 50 60 70 80
CGKKEAAPAS ASEPAASSA QGDTSSIGST MQQASYAMGV DIGRSLKQMK EQGAEIDLKV

m576.pep
40 50 60 70 80 90
FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA
|||||
a576
90 100 110 120 130 140
FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA

m576.pep
100 110 120 130 140 150
KDGVTTSAG LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
|||||
a576
150 160 170 180 190 200
KDGVTTSAG LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ

m576.pep
160 170 180 190 200 210
VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
|||||
a576
210 220 230 240 250 260
VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA

m576.pep
220
KQPAQVDIKK VN*
|||||
a576
270
KQPAQVDIKK VN*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCAGCATC GCATCCGAAC
101 CTGCCGCGCG TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTACCGATG
251 CCATGCAGGC AGTGATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGCT
451 CTGCAGTACA AAATACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GCGCGCCCGG CCACCTTCCC TTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCCGCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTACCGAAG
251 CCATGCAGGC AGTGATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGCGCGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLEKGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	250	260	270			
	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCCAAA AAGAAGCCGC CCCC GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCAG
701 GCGCAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGV LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1   atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttattttacg gagcaaacat gaaacttatc tataccgtca tcaaaatcat
201 tatectgctg ctcttctctg tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cggttgctgt cggcacgtg ttcggaatgt ttgccctgtt
351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1   MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRSCPCGV
51  FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTFSYLPQ QSVNPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1   ATGGAAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCCTA CTGCGCGGGG CAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTTGTAGT CCGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1   MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGCV
51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
          |||:|||||
g577      MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLTQSWFRVRSCPCGVFIYGANMKLI
          10      20      30      40      50      60

      70      80      90     100     110     120
m577.pep  YTVIKIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
```

895

```

g577      |||||:|||||:|||||:|||||:|||||:
          YTVIKIIILLFLLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
          70      80      90      100     110     120

          130      140      150      160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||:
g577      LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKQFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1  ATGGAAAGGA  ACGGTGTATT  TGGTAAAATT  GTCGGCAATC  GCATACTCCG
51  TATGTCGTCC  GAACACGCTG  CCGCATCCTA  TCCGAAACCG  TGCAAATCGT
101 TTAAACTAGC  GCAATCTTGG  TTCAGAGTGC  GAAGCTGTCC  GGGCGGCGTT
151 TTTATTTACG  GAGCAAACAT  GAAACTTATC  TATACCGTCA  TCAAAATCAT
201 TATCCTGCTG  CTCTCCTGCT  TGCTTGCTGT  CATTAATACG  GATGCCGTTA
251 CCTTTTCCTA  CCTGCCGGGG  CAAAATTCG  ATTTGCCGCT  GATTGTCGTA
301 TTGTTCCGGC  CGTTTGTCTG  CGGCATCGTG  TTCGGAATGT  TTGCCTTGTT
351 CGGACGGTTG  TTGTCGTTAC  GTGGCGAGAA  CGGCAGGTTG  CGTGCCGAAG
401 TAAAGAAAAA  TGC GCGTTT  AC GGGGAAGG  AGCTGACCGC  ACCACCGGCG
451 CAAAATGCGC  CCGAATCTGC  CAAACAGCCT  TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.pep
1  MERNGVFGKI  VGNRILRMSS  EHAAASYPKP  CKSFKLAQSW  FRVRSCPGGV
51  FIYGANMKLI  YTVIKIIILL  LFLLLAVINT  DAVTFSYLPQ  QKFDLPLIVV
101 LFGAFVVGIV  FGMFALFGRL  LSLRGENGR  LRAEVKKNAR  LGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

          10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCPGGVFIYGANMKLI
          |||||:|||||:|||||:|||||:|||||:
a577      MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCPGGVFIYGANMKLI
          10      20      30      40      50      60

          70      80      90      100     110     120
m577.pep  YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
          |||||:|||||:|||||:|||||:|||||:
a577      YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
          70      80      90      100     110     120

          130      140      150      160
m577.pep  LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          |||||:|||||:|||||:|||||:|||||:
a577      LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq
1  atgggaaagc  tcgacatcgg  gatattgttt  gccgatttct  tcaaagattt
51  cgcgccacag  ttcggtggtt  tccaaaacgt  tggctttgcc  tacggagcag
101 acttttttgc  tgcgtttttg  ggcggattgg  aaggccacgt  gggcgatgcg
151 gcggtttcgc  ctttcgctgt  atttcattgt  gttgtagcct  tcgtgttcgc
201 cgtttttcaa  aacacggatg  cgcgcgggtt  cgccgaaata  aatatcgccg
251 gtaagttcgc  gcacaatcaa  aatatccaaa  ccggcaacga  tttcaggctt
301 gagcgtggag  gcgttggtta  a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.pep
1  MGKLDIGILF  ADFFKDFAPQ  FGGFQNVGFA  YGADFFAAFL  GGLEGHVGDA
51  ADFAFAVFGH  VVAFVFAVFQ  NTDAARFAEI  NIAGKFAHNQ  NIQTGNDFRL

```

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTTGC TGCCTTTTGG GCGGATTGG AAGGCAACAT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGGCAACGA TTTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMGNT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	: : :					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : :					
g578	VVAFAFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTTGC TGCCTTTTGG GCGGATTGG AAGGCGACGT GGGCAATACG
151 GCGGATTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADEFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMGNTADFAFAVFHG					
	: : :					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : :					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```

```

51   TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101  CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151  GGCGCGGGTT TGGCGGTGGC GTTGTCCCTA AAAGACCAGC TGTCCAATTT
201  TGCCGCGGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGACT
251  TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301  CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351  CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401  GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451  AAAGAGGCGG TGTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501  CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551  TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601  CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651  CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

```

g579.pep..
1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAAYITALG DNAIEITLWA WANEADRRTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

```

m579.seq..
1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCGGGC GCACTGATTA TCCTGTTCCG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

```

m579.pep..
1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRRTL
201 QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m579/g579 98.7% identity in 231 aa overlap

      10      20      30      40      50      60
m579.pep  MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          |||
g579       MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL
          |||

      70      80      90     100     110     120
m579.pep  KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
          |||
g579       KDQLSNFAAGALIIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
          |||

      70      80      90     100     110     120

```

898

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	: : : : :					
g579	DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```

a579.seq
1   ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GGCGCGGGTT TGGCGGTGGC GTTGCTCTTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCG CCCGTTCAA A GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAATGGTG
301 CAGACTTCTT TGGCGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCCGCCG CCTACATCAC CGCCTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```

a579.pep
1   MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51  GAGLAVALSI KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLRTDNE EVVLPNSVVM GNSIVNRSTL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

m579/a579 100.0% identity in 231 aa overlap

10      20      30      40      50      60
m579.pep MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSI
|||||
a579      MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSI
10      20      30      40      50      60

70      80      90      100     110     120
m579.pep KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
|||||
a579      KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM
70      80      90      100     110     120

130     140     150     160     170     180
m579.pep GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
|||||
a579      GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG
130     140     150     160     170     180

190     200     210     220     230
m579.pep DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
|||||
a579      DNAIEITLWAWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:
g579-1.seq